

DT05 Rec'd PCT/PTO 17 FEB 2005

## SEQUENCE LISTING

5 <110> SunGene GmbH Co. KGaA

<120> Use of astaxanthin-containing plants or parts of plants of the ge-  
10 nus Tagetes as feedstuffs

<130> PF 54148  
15

<160> 142

20

<170> PatentIn version 3.1

25

<210> 1

<211> 1771

30 <212> DNA

<213> Haematococcus pluvialis

35

<220>

<221> CDS

40 <222> (166)..(1155)

<223>

45

BEST AVAILABLE COPY

&lt;400&gt; 1

1 ggacacgagct tgcacgcaag tcagcgcgcg caagtcaaca cctgccggtc cacagcctca 60  
 aataataaag agctcaagcg tttgtgcgcc tcgacgtggc cagtctgcac tgccttgaac 120  
 5 ccgcgagtct cccgccgcac tgactgccat agcacagcta gacga atg cag cta gca 177  
 Met Gln Leu Ala  
 1  
 10 gcg aca gta atg ttg gag cag ctt acc gga agc gct gag gca ctc aag 225  
 Ala Thr Val Met Leu Glu Gln Leu Thr Gly Ser Ala Glu Ala Leu Lys  
 5 10 15 20  
 gag aag gag aag gag gtt gca ggc agc tct gac gtg ttg cgt aca tgg 273  
 15 Glu Lys Glu Lys Glu Val Ala Gly Ser Ser Asp Val Leu Arg Thr Trp  
 25 30 35  
 gcg acc cag tac tcg ctt ccg tca gaa gag tca gac gcg gcc cgc ccg 321  
 Ala Thr Gln Tyr Ser Leu Pro Ser Glu Glu Ser Asp Ala Ala Arg Pro  
 20 40 45 50  
 gga ctg aag aat gcc tac aag cca cca cct tcc gac aca aag ggc atc 369  
 Gly Leu Lys Asn Ala Tyr Lys Pro Pro Pro Ser Asp Thr Lys Gly Ile  
 55 60 65  
 25 aca atg gcg cta cgt gtc atc ggc tcc tgg gcc gca gtg ttc ctc cac 417  
 Thr Met Ala Leu Arg Val Ile Gly Ser Trp Ala Ala Val Phe Leu His  
 70 75 80  
 30 gcc att ttt caa atc aag ctt ccg acc tcc ttg gac cag ctg cac tgg 465  
 Ala Ile Phe Gln Ile Lys Leu Pro Thr Ser Leu Asp Gln Leu His Trp  
 85 90 95 100  
 ctg ccc gtg tca gat gcc aca gct cag ctg gtt agc ggc acg agc agc 513  
 35 Leu Pro Val Ser Asp Ala Thr Ala Gln Leu Val Ser Gly Thr Ser Ser  
 105 110 115  
 ctg ctc gac atc gtc gta gta ttc ttt gtc ctg gag ttc ctg tac aca 561  
 Leu Leu Asp Ile Val Val Val Phe Phe Val Leu Glu Phe Leu Tyr Thr  
 40 120 125 130  
 ggc ctt ttt atc acc acg cat gat gct atg cat ggc acc atc gcc atg 609  
 Gly Leu Phe Ile Thr Thr His Asp Ala Met His Gly Thr Ile Ala Met  
 135 140 145

45

	aga aac agg cag ctt aat gac ttc ttg ggc aga gta tgc atc tcc ttg	657
	Arg Asn Arg Gln Leu Asn Asp Phe Leu Gly Arg Val Cys Ile Ser Leu	
	150 155 160	
5	tac gcc tgg ttt gat tac aac atg ctg cac cgc aag cat tgg gag cac	705
	Tyr Ala Trp Phe Asp Tyr Asn Met Leu His Arg Lys His Trp Glu His	
	165 170 175 180	
	cac aac cac act ggc gag gtg ggc aag gac cct gac ttc cac agg gga	753
10	His Asn His Thr Gly Glu Val Gly Lys Asp Pro Asp Phe His Arg Gly	
	185 190 195	
	aac cct ggc att gtg ccc tgg ttt gcc agc ttc atg tcc agc tac atg	801
15	Asn Pro Gly Ile Val Pro Trp Phe Ala Ser Phe Met Ser Ser Tyr Met	
	200 205 210	
	tcg atg tgg cag ttt gcg cgc ctc gca tgg tgg acg gtg gtc atg cag	849
	Ser Met Trp Gln Phe Ala Arg Leu Ala Trp Trp Thr Val Val Met Gln	
	215 220 225	
20	ctg ctg ggt gcg cca atg gcg aac ctg ctg gtg ttc atg gcg gcc gcg	897
	Leu Leu Gly Ala Pro Met Ala Asn Leu Leu Val Phe Met Ala Ala Ala	
	230 235 240	
25	ccc atc ctg tcc gcc ttc cgc ttg ttc tac ttt ggc acg tac atg ccc	945
	Pro Ile Leu Ser Ala Phe Arg Leu Phe Tyr Phe Gly Thr Tyr Met Pro	
	245 250 255 260	
	cac aag cct gag cct ggc gcc gcg tca ggc tct tca cca gcc gtc atg	993
30	His Lys Pro Glu Pro Gly Ala Ala Ser Gly Ser Ser Pro Ala Val Met	
	265 270 275	
	aac tgg tgg aag tcg cgc act agc cag gcg tcc gac ctg gtc agc ttt	1041
	Asn Trp Trp Lys Ser Arg Thr Ser Gln Ala Ser Asp Leu Val Ser Phe	
35	280 285 290	
	ctg acc tgc tac cac ttc gac ctg cac tgg gag cac cac cgc tgg ccc	1089
	Leu Thr Cys Tyr His Phe Asp Leu His Trp Glu His His Arg Trp Pro	
	295 300 305	
40	ttc gcc ccc tgg tgg gag ctg ccc aac tgc cgc cgc ctg tct ggc cga	1137
	Phe Ala Pro Trp Trp Glu Leu Pro Asn Cys Arg Arg Leu Ser Gly Arg	
	310 315 320	
45	ggc ctg gtt cct gcc tag ctggacacac tgcagtgggc cctgctgcca	1185

Gly Leu Val Pro Ala

325

5 gctgggcatg caggttgtgg caggactggg tgagggtgaaa agctgcaggc gctgctgccg 1245  
 gagacgctgc atgggctacc ctgtgtagct gccgccacta ggggaggggg tttgtagctg 1305  
 tcgagcttgc cccatggatg aagctgtgta gtggtgcagg gactacaccc acaggccaac 1365  
 10 acccttgcag gagatgtctt gcgtcgggag gagtgttggg cagtgtagat gctatgattg 1425  
 tatcttaatg ctgaagcctt taggggagcg acacttagtg ctgggcaggc aacgccctgc 1485  
 aagggtgcagg cacaagctag gctggacgag gactcgggtg caggcagggtg aagaggtgcg 1545  
 15 ggaggggtgg gccacacca ctgggcaaga ccatgctgca atgctggcgg tgtggcagtg 1605  
 agagctgcgt gattaactgg gctatggatt gtttgagcag tctcacttat tctttgatat 1665  
 20 agatactggg caggcaggtc aggagagtga gtatgaacaa gttgagaggt ggtgcgctgc 1725  
 ccctgcgctt atgaagctgt aacaataaag tgggtcaaaa aaaaaa 1771

25 &lt;210&gt; 2

&lt;211&gt; 329

&lt;212&gt; PRT

30

&lt;213&gt; Haematococcus pluvialis

35 &lt;400&gt; 2

Met Gln Leu Ala Ala Thr Val Met Leu Glu Gln Leu Thr Gly Ser Ala

1

5

10

15

40

Glu Ala Leu Lys Glu Lys Glu Lys Glu Val Ala Gly Ser Ser Asp Val

20

25

30

45 Leu Arg Thr Trp Ala Thr Gln Tyr Ser Leu Pro Ser Glu Glu Ser Asp



35

40

45

Ala Ala Arg Pro Gly Leu Lys Asn Ala Tyr Lys Pro Pro Pro Ser Asp  
 5 50 55 60

Thr Lys Gly Ile Thr Met Ala Leu Arg Val Ile Gly Ser Trp Ala Ala  
 65 70 75 80

Val Phe Leu His Ala Ile Phe Gln Ile Lys Leu Pro Thr Ser Leu Asp  
 85 90 95

Gln Leu His Trp Leu Pro Val Ser Asp Ala Thr Ala Gln Leu Val Ser  
 100 105 110

Gly Thr Ser Ser Leu Leu Asp Ile Val Val Val Phe Phe Val Leu Glu  
 115 120 125

Phe Leu Tyr Thr Gly Leu Phe Ile Thr Thr His Asp Ala Met His Gly  
 130 135 140

Thr Ile Ala Met Arg Asn Arg Gln Leu Asn Asp Phe Leu Gly Arg Val  
 145 150 155 160

Cys Ile Ser Leu Tyr Ala Trp Phe Asp Tyr Asn Met Leu His Arg Lys  
 165 170 175

His Trp Glu His His Asn His Thr Gly Glu Val Gly Lys Asp Pro Asp  
 180 185 190

Phe His Arg Gly Asn Pro Gly Ile Val Pro Trp Phe Ala Ser Phe Met  
 195 200 205

Ser Ser Tyr Met Ser Met Trp Gln Phe Ala Arg Leu Ala Trp Trp Thr  
 210 215 220

Val Val Met Gln Leu Leu Gly Ala Pro Met Ala Asn Leu Leu Val Phe  
225 230 235 240

5 Met Ala Ala Ala Pro Ile Leu Ser Ala Phe Arg Leu Phe Tyr Phe Gly  
245 250 255

10 Thr Tyr Met Pro His Lys Pro Glu Pro Gly Ala Ala Ser Gly Ser Ser  
260 265 270

15 Pro Ala Val Met Asn Trp Trp Lys Ser Arg Thr Ser Gln Ala Ser Asp  
275 280 285

20 Leu Val Ser Phe Leu Thr Cys Tyr His Phe Asp Leu His Trp Glu His  
290 295 300

25 His Arg Trp Pro Phe Ala Pro Trp Trp Glu Leu Pro Asn Cys Arg Arg  
305 310 315 320

Leu Ser Gly Arg Gly Leu Val Pro Ala  
325

30 <210> 3  
<211> 1662

35 <212> DNA  
<213> Haematococcus pluvialis

40 <220>  
<221> CDS

&lt;222&gt; (168)..(1130)

&lt;223&gt;

5

&lt;400&gt; 3

	cggggcaact caagaaattc aacagctgca agcgcgcccc agcctcacag cgccaagtga	60
10	gctatcgacg tggttgtgag cgctcgacgt ggtccactga cgggcctgtg agcctctgag	120
	ctccgtcctc tgccaaatct cgcgtcgggg cctgcctaag tcgaaga atg cac gtc	176
		Met His Val
		1
15	gca tcg gca cta atg gtc gag cag aaa ggc agt gag gca gct gct tcc	224
	Ala Ser Ala Leu Met Val Glu Gln Lys Gly Ser Glu Ala Ala Ala Ser	
	5 10 15	
20	agc cca gac gtc ttg aga gcg tgg gcg aca cag tat cac atg cca tcc	272
	Ser Pro Asp Val Leu Arg Ala Trp Ala Thr Gln Tyr His Met Pro Ser	
	20 25 30 35	
	gag tcg tca gac gca gct cgt cct gcg cta aag cac gcc tac aaa cct	320
25	Glu Ser Ser Asp Ala Ala Arg Pro Ala Leu Lys His Ala Tyr Lys Pro	
	40 45 50	
	cca gca tct gac gcc aag ggc atc acg atg gcg ctg acc atc att ggc	368
	Pro Ala Ser Asp Ala Lys Gly Ile Thr Met Ala Leu Thr Ile Ile Gly	
30	55 60 65	
	acc tgg acc gca gtg ttt tta cac gca ata ttt caa atc agg cta ccg	416
	Thr Trp Thr Ala Val Phe Leu His Ala Ile Phe Gln Ile Arg Leu Pro	
	70 75 80	
35	aca tcc atg gac cag ctt cac tgg ttg cct gtg tcc gaa gcc aca gcc	464
	Thr Ser Met Asp Gln Leu His Trp Leu Pro Val Ser Glu Ala Thr Ala	
	85 90 95	
40	cag ctt ttg ggc gga agc agc agc cta ctg cac atc gct gca gtc ttc	512
	Gln Leu Leu Gly Gly Ser Ser Ser Leu Leu His Ile Ala Ala Val Phe	
	100 105 110 115	
	att gta ctt gag ttc ctg tac act ggt cta ttc atc acc aca cat gac	560
45	Ile Val Leu Glu Phe Leu Tyr Thr Gly Leu Phe Ile Thr Thr His Asp	

	120	125	130	
	gca atg cat ggc acc ata gct ttg agg cac agg cag ctc aat gat ctc			608
	Ala Met His Gly Thr Ile Ala Leu Arg His Arg Gln Leu Asn Asp Leu			
5	135	140	145	
	ctt ggc aac atc tgc ata tca ctg tac gcc tgg ttt gac tac agc atg			656
	Leu Gly Asn Ile Cys Ile Ser Leu Tyr Ala Trp Phe Asp Tyr Ser Met			
	150	155	160	
10	ctg cat cgc aag cac tgg gag cac cac aac cat act ggc gaa gtg ggg			704
	Leu His Arg Lys His Trp Glu His His Asn His Thr Gly Glu Val Gly			
	165	170	175	
15	aaa gac cct gac ttc cac aag gga aat ccc ggc ctt gtc ccc tgg ttc			752
	Lys Asp Pro Asp Phe His Lys Gly Asn Pro Gly Leu Val Pro Trp Phe			
	180	185	190	195
	gcc agc ttc atg tcc agc tac atg tcc ctg tgg cag ttt gcc cgg ctg			800
20	Ala Ser Phe Met Ser Ser Tyr Met Ser Leu Trp Gln Phe Ala Arg Leu			
	200	205	210	
	gca tgg tgg gca gtg gtg atg caa atg ctg ggg gcg ccc atg gca aat			848
	Ala Trp Trp Ala Val Val Met Gln Met Leu Gly Ala Pro Met Ala Asn			
25	215	220	225	
	ctc cta gtc ttc atg gct gca gcc cca atc ttg tca gca ttc cgc ctc			896
	Leu Leu Val Phe Met Ala Ala Ala Pro Ile Leu Ser Ala Phe Arg Leu			
	230	235	240	
30	ttc tac ttc ggc act tac ctg cca cac aag cct gag cca ggc cct gca			944
	Phe Tyr Phe Gly Thr Tyr Leu Pro His Lys Pro Glu Pro Gly Pro Ala			
	245	250	255	
35	gca ggc tct cag gtg atg gcc tgg ttc agg gcc aag aca agt gag gca			992
	Ala Gly Ser Gln Val Met Ala Trp Phe Arg Ala Lys Thr Ser Glu Ala			
	260	265	270	275
	tct gat gtg atg agt ttc ctg aca tgc tac cac ttt gac ctg cac tgg			1040
40	Ser Asp Val Met Ser Phe Leu Thr Cys Tyr His Phe Asp Leu His Trp			
	280	285	290	
	gag cac cac agg tgg ccc ttt gcc ccc tgg tgg cag ctg ccc cac tgc			1088
	Glu His His Arg Trp Pro Phe Ala Pro Trp Trp Gln Leu Pro His Cys			
45	295	300	305	

'cgc cgc ctg tcc ggg cgt ggc ctg gtg cct gcc ttg gca tga 1130  
 Arg Arg Leu Ser Gly Arg Gly Leu Val Pro Ala Leu Ala  
 310 315 320

5

cctggtccct ccgctggtga cccagcgtct gcacaagagt gtcattgctac aggggtgctgc 1190  
 ggccagtggc agcgcagtgc actctcagcc tgtatggggc taccgctgtg ccactgagca 1250

10

ctgggcatgc cactgagcac tgggcgtgct actgagcaat gggcgtgcta ctgagcaatg 1310  
 ggcgtgctac tgacaatggg cgtgctactg gggctctggca gtggctagga tggagtttga 1370  
 tgcattcagt agcgggtggc aacgtcatgt ggatggtgga agtgctgagg ggtttaggca 1430

15

gccggcattt gagagggcta agttataaat cgcattgctgc tcatgcgcac atatctgcac 1490  
 acagccaggg aaatcccttc gagagtgatt atgggacact tgtattggtt tcgtgctatt 1550

20

gttttattca gcagcagtac ttagtgaggg tgagagcagg gtggtgagag tggagtgagt 1610  
 gagtatgaac ctggtcagcg aggtgaacag cctgtaatga atgactctgt ct 1662

25

<210> 4  
 <211> 320  
 <212> PRT

30

<213> Haematococcus pluvialis

35

<400> 4  
 Met His Val Ala Ser Ala Leu Met Val Glu Gln Lys Gly Ser Glu Ala  
 1 5 10 15

40

Ala Ala Ser Ser Pro Asp Val Leu Arg Ala Trp Ala Thr Gln Tyr His  
 20 25 30

45

Met Pro Ser Glu Ser Ser Asp Ala Ala Arg Pro Ala Leu Lys His Ala

35 40 45  
 Tyr Lys Pro Pro Ala Ser Asp Ala Lys Gly Ile Thr Met Ala Leu Thr  
 5 50 55 60  
 Ile Ile Gly Thr Trp Thr Ala Val Phe Leu His Ala Ile Phe Gln Ile  
 65 70 75 80  
 10  
 Arg Leu Pro Thr Ser Met Asp Gln Leu His Trp Leu Pro Val Ser Glu  
 85 90 95  
 15  
 Ala Thr Ala Gln Leu Leu Gly Gly Ser Ser Ser Leu Leu His Ile Ala  
 100 105 110  
 20  
 Ala Val Phe Ile Val Leu Glu Phe Leu Tyr Thr Gly Leu Phe Ile Thr  
 115 120 125  
 25  
 Thr His Asp Ala Met His Gly Thr Ile Ala Leu Arg His Arg Gln Leu  
 130 135 140  
 30  
 Asn Asp Leu Leu Gly Asn Ile Cys Ile Ser Leu Tyr Ala Trp Phe Asp  
 145 150 155 160  
 Tyr Ser Met Leu His Arg Lys His Trp Glu His His Asn His Thr Gly  
 165 170 175  
 35  
 Glu Val Gly Lys Asp Pro Asp Phe His Lys Gly Asn Pro Gly Leu Val  
 180 185 190  
 40  
 Pro Trp Phe Ala Ser Phe Met Ser Ser Tyr Met Ser Leu Trp Gln Phe  
 195 200 205  
 45  
 Ala Arg Leu Ala Trp Trp Ala Val Val Met Gln Met Leu Gly Ala Pro  
 210 215 220

Met Ala Asn Leu Leu Val Phe Met Ala Ala Ala Pro Ile Leu Ser Ala  
 225 230 235 240  
 5

Phe Arg Leu Phe Tyr Phe Gly Thr Tyr Leu Pro His Lys Pro Glu Pro  
 245 250 255

10 Gly Pro Ala Ala Gly Ser Gln Val Met Ala Trp Phe Arg Ala Lys Thr  
 260 265 270

15 Ser Glu Ala Ser Asp Val Met Ser Phe Leu Thr Cys Tyr His Phe Asp  
 275 280 285

20 Leu His Trp Glu His His Arg Trp Pro Phe Ala Pro Trp Trp Gln Leu  
 290 295 300

25 Pro His Cys Arg Arg Leu Ser Gly Arg Gly Leu Val Pro Ala Leu Ala  
 305 310 315 320

<210> 5

30 <211> 729

<212> DNA

<213> Agrobacterium aurantiacum

35

<220>

<221> CDS

40 <222> (1) .. (729)

<223>

<400> 5  
 atg agc gca cat gcc ctg ccc aag gca gat ctg acc gcc acc agc ctg 48  
 5 Met Ser Ala His Ala Leu Pro Lys Ala Asp Leu Thr Ala Thr Ser Leu  
 1 5 10 15

atc gtc tcg ggc ggc atc atc gcc gct tgg ctg gcc ctg cat gtg cat 96  
 10 Ile Val Ser Gly Gly Ile Ile Ala Ala Trp Leu Ala Leu His Val His  
 20 25 30

gcg ctg tgg ttt ctg gac gca gcg gcg cat ccc atc ctg gcg atc gca 144  
 Ala Leu Trp Phe Leu Asp Ala Ala Ala His Pro Ile Leu Ala Ile Ala  
 35 40 45  
 15

aat ttc ctg ggg ctg acc tgg ctg tcg gtc gga ttg ttc atc atc gcg 192  
 Asn Phe Leu Gly Leu Thr Trp Leu Ser Val Gly Leu Phe Ile Ile Ala  
 50 55 60

cat gac gcg atg cac ggg tcg gtg gtg ccg ggg cgt ccg cgc gcc aat 240  
 20 His Asp Ala Met His Gly Ser Val Val Pro Gly Arg Pro Arg Ala Asn  
 65 70 75 80

gcg gcg atg ggc cag ctt gtc ctg tgg ctg tat gcc gga ttt tcg tgg 288  
 25 Ala Ala Met Gly Gln Leu Val Leu Trp Leu Tyr Ala Gly Phe Ser Trp  
 85 90 95

cgc aag atg atc gtc aag cac atg gcc cat cac cgc cat gcc gga acc 336  
 Arg Lys Met Ile Val Lys His Met Ala His His Arg His Ala Gly Thr  
 30 100 105 110

gac gac gac ccg gat ttc gac cat ggc ggc ccg gtc cgc tgg tac gcc 384  
 Asp Asp Asp Pro Asp Phe Asp His Gly Gly Pro Val Arg Trp Tyr Ala  
 115 120 125  
 35

cgc ttc atc ggc acc tat ttc ggc tgg cgc gag ggg ctg ctg ctg ccc 432  
 Arg Phe Ile Gly Thr Tyr Phe Gly Trp Arg Glu Gly Leu Leu Leu Pro  
 130 135 140

gtc atc gtg acg gtc tat gcg ctg atc ctt ggg gat cgc tgg atg tac 480  
 40 Val Ile Val Thr Val Tyr Ala Leu Ile Leu Gly Asp Arg Trp Met Tyr  
 145 150 155 160

gtg gtc ttc tgg ccg ctg ccg tcg atc ctg gcg tcg atc cag ctg ttc 528  
 45 Val Val Phe Trp Pro Leu Pro Ser Ile Leu Ala Ser Ile Gln Leu Phe



	165	170	175			
5	gtg ttc ggc acc tgg ctg ccg cac cgc ccc ggc cac gac gcg ttc ccg Val Phe Gly Thr Trp Leu Pro His Arg Pro Gly His Asp Ala Phe Pro	180	185	190	576	
10	gac cgc cac aat gcg cgg tcg tcg cgg atc agc gac ccc gtg tcg ctg Asp Arg His Asn Ala Arg Ser Ser Arg Ile Ser Asp Pro Val Ser Leu	195	200	205	624	
15	ctg acc tgc ttt cac ttt ggc ggt tat cat cac gaa cac cac ctg cac Leu Thr Cys Phe His Phe Gly Gly Tyr His His Glu His His Leu His	210	215	220	672	
20	ccg acg gtg ccg tgg tgg cgc ctg ccc agc acc cgc acc aag ggg gac Pro Thr Val Pro Trp Trp Arg Leu Pro Ser Thr Arg Thr Lys Gly Asp	225	230	235	240	720
25	acc gca tga Thr Ala				729	
30	<210> 6 <211> 242 <212> PRT <213> Agrobacterium aurantiacum					
35	<400> 6 Met Ser Ala His Ala Leu Pro Lys Ala Asp Leu Thr Ala Thr Ser Leu	1	5	10	15	
40	Ile Val Ser Gly Gly Ile Ile Ala Ala Trp Leu Ala Leu His Val His	20	25	30		
45	Ala Leu Trp Phe Leu Asp Ala Ala Ala His Pro Ile Leu Ala Ile Ala	35	40	45		

5      Asn Phe Leu Gly Leu Thr Trp Leu Ser Val Gly Leu Phe Ile Ile Ala  
        50                                 55                                 60

10     His Asp Ala Met His Gly Ser Val Val Pro Gly Arg Pro Arg Ala Asn  
        65                                 70                                 75                                 80

15     Ala Ala Met Gly Gln Leu Val Leu Trp Leu Tyr Ala Gly Phe Ser Trp  
                                85                                 90                                 95

20     Arg Lys Met Ile Val Lys His Met Ala His His Arg His Ala Gly Thr  
                                100                                 105                                 110

25     Asp Asp Asp Pro Asp Phe Asp His Gly Gly Pro Val Arg Trp Tyr Ala  
                                115                                 120                                 125

30     Arg Phe Ile Gly Thr Tyr Phe Gly Trp Arg Glu Gly Leu Leu Leu Pro  
                                130                                 135                                 140

35     Val Ile Val Thr Val Tyr Ala Leu Ile Leu Gly Asp Arg Trp Met Tyr  
                                145                                 150                                 155                                 160

40     Val Val Phe Trp Pro Leu Pro Ser Ile Leu Ala Ser Ile Gln Leu Phe  
                                165                                 170                                 175

45     Val Phe Gly Thr Trp Leu Pro His Arg Pro Gly His Asp Ala Phe Pro  
                                180                                 185                                 190

50     Asp Arg His Asn Ala Arg Ser Ser Arg Ile Ser Asp Pro Val Ser Leu  
                                195                                 200                                 205

55     Leu Thr Cys Phe His Phe Gly Gly Tyr His His Glu His His Leu His  
                                210                                 215                                 220

Pro Thr, Val Pro Trp Trp Arg Leu Pro Ser Thr Arg Thr Lys Gly Asp  
225 230 235 240

5

Thr Ala

10

<210> 7

<211> 1631

<212> DNA

15

<213> Alcaligenes sp.

20

<220>

<221> CDS

<222> (99) .. (827)

25

<223>

30

<400> 7

ctgcaggccg ggcccgggtgg ccaatgggtcg caaccggcag gactggaaca ggacggcggg 60

ccgggtctagg ctgtcgccct acgcagcagg agtttcgg atg tcc gga cgg aag cct 116

Met Ser Gly Arg Lys Pro

35

1

5

ggc aca act ggc gac acg atc gtc aat ctc ggt ctg acc gcc gcg atc 164

Gly Thr Thr Gly Asp Thr Ile Val Asn Leu Gly Leu Thr Ala Ala Ile

10

15

20

40

ctg ctg tgc tgg ctg gtc ctg cac gcc ttt acg cta tgg ttg cta gat 212

Leu Leu Cys Trp Leu Val Leu His Ala Phe Thr Leu Trp Leu Leu Asp

25

30

35

45

gcg gcc gcg cat ccg ctg ctt gcc gtg ctg tgc ctg gct ggg ctg acc 260

	Ala Ala Ala His Pro Leu Leu Ala Val Leu Cys Leu Ala Gly Leu Thr	
	40 45 50	
5	tgg ctg tgc gtc ggg ctg ttc atc atc gcg cat gac gca atg cac ggg Trp Leu Ser Val Gly Leu Phe Ile Ile Ala His Asp Ala Met His Gly	308
	55 60 65 70	
10	tcc gtg gtg ccg ggg cgg ccg cgc gcc aat gcg gcg atc ggg caa ctg Ser Val Val Pro Gly Arg Pro Arg Ala Asn Ala Ala Ile Gly Gln Leu	356
	75 80 85	
15	gcg ctg tgg ctc tat gcg ggg ttc tgc tgg ccc aag ctg atc gcc aag Ala Leu Trp Leu Tyr Ala Gly Phe Ser Trp Pro Lys Leu Ile Ala Lys	404
	90 95 100	
	cac atg acg cat cac cgg cac gcc ggc acc gac aac gat ccc gat ttc His Met Thr His His Arg His Ala Gly Thr Asp Asn Asp Pro Asp Phe	452
	105 110 115	
20	ggt cac gga ggg ccc gtg cgc tgg tac ggc agc ttc gtc tcc acc tat Gly His Gly Gly Pro Val Arg Trp Tyr Gly Ser Phe Val Ser Thr Tyr	500
	120 125 130	
25	ttc ggc tgg cga gag gga ctg ctg cta ccg gtg atc gtc acc acc tat Phe Gly Trp Arg Glu Gly Leu Leu Leu Pro Val Ile Val Thr Thr Tyr	548
	135 140 145 150	
30	gcg ctg atc ctg ggc gat cgc tgg atg tat gtc atc ttc tgg ccg gtc Ala Leu Ile Leu Gly Asp Arg Trp Met Tyr Val Ile Phe Trp Pro Val	596
	155 160 165	
35	ccg gcc gtt ctg gcg tgc atc cag att ttc gtc ttc gga act tgg ctg Pro Ala Val Leu Ala Ser Ile Gln Ile Phe Val Phe Gly Thr Trp Leu	644
	170 175 180	
	ccc cac cgc ccg gga cat gac gat ttt ccc gac cgg cac aac gcg agg Pro His Arg Pro Gly His Asp Asp Phe Pro Asp Arg His Asn Ala Arg	692
	185 190 195	
40	tgc acc ggc atc ggc gac ccg ttg tca cta ctg acc tgc ttc cat ttc Ser Thr Gly Ile Gly Asp Pro Leu Ser Leu Leu Thr Cys Phe His Phe	740
	200 205 210	
45	ggc ggc tat cac cac gaa cat cac ctg cat ccg cat gtg ccg tgg tgg Gly Gly Tyr His His Glu His His Leu His Pro His Val Pro Trp Trp	788

	215	220	225	230	
	cgc ctg cct cgt aca cgc aag acc gga ggc cgc gca tga cgcaattcct				837
	Arg Leu Pro Arg Thr Arg Lys Thr Gly Gly Arg Ala				
5		235	240		
	cattgtcgtg gcgacagtcc tcgtgatgga gctgaccgcc tattccgtcc accgctggat				897
	tatgcacggc cccctaggct ggggctggca caagtcccat cacgaagagc acgaccacgc				957
10	gttggagaag aacgacctct acggcgtcgt cttcgcggtg ctggcgacga tcctcttcac				1017
	cgtgggcgcc tattggtggc cggtgctgtg gtggatcgcc ctgggcatga cggctctatgg				1077
15	gttgatctat ttcatacctgc acgacgggct tgtgcatcaa cgctggccgt ttcggtatat				1137
	tccgcggcgg ggctatttcc gcaggctcta ccaagctcat cgcctgcacc acgcggtcga				1197
	ggggcgggac cactgcgtca gcttcggctt catctatgcc ccaccctgg acaagctgaa				1257
20	gcaggatctg aagcggtcgg gtgtcctgcg cccccaggac gagcgtccgt cgtgatctct				1317
	gatccccggcg tggccgcatg aaatccgacg tgctgctggc aggggcccgc cttgccaacg				1377
25	gactgatcgc gctggcgatc cgcaaggcgc ggcccgaacct tcgcgtgctg ctgctggacc				1437
	gtgcggcggg cgcctcggac gggcatactt ggtcctgcc aacacccgat ttggcgccgc				1497
	actggctgga ccgcctgaag ccgatcaggc gtggcgactg gcccgatcag gaggtgcggt				1557
30	tcccagacca ttcgcgaagg ctccgggccc gatatggctc gatcgacggg cgggggctga				1617
	tgctgceggg gacc				1631
35					
	<210>	8			
	<211>	242			
40	<212>	PRT			
	<213>	Alcaligenes sp.			
45					

&lt;400&gt; 8

Met Ser Gly Arg Lys Pro Gly Thr Thr Gly Asp Thr Ile Val Asn Leu  
 1 5 10 15  
 5

Gly Leu Thr Ala Ala Ile Leu Leu Cys Trp Leu Val Leu His Ala Phe  
 20 25 30  
 10

Thr Leu Trp Leu Leu Asp Ala Ala Ala His Pro Leu Leu Ala Val Leu  
 35 40 45  
 15

Cys Leu Ala Gly Leu Thr Trp Leu Ser Val Gly Leu Phe Ile Ile Ala  
 50 55 60  
 20

His Asp Ala Met His Gly Ser Val Val Pro Gly Arg Pro Arg Ala Asn  
 65 70 75 80  
 25

Ala Ala Ile Gly Gln Leu Ala Leu Trp Leu Tyr Ala Gly Phe Ser Trp  
 85 90 95  
 30

Pro Lys Leu Ile Ala Lys His Met Thr His His Arg His Ala Gly Thr  
 100 105 110  
 35

Asp Asn Asp Pro Asp Phe Gly His Gly Gly Pro Val Arg Trp Tyr Gly  
 115 120 125  
 40

Ser Phe Val Ser Thr Tyr Phe Gly Trp Arg Glu Gly Leu Leu Leu Pro  
 130 135 140  
 45

Val Ile Val Thr Thr Tyr Ala Leu Ile Leu Gly Asp Arg Trp Met Tyr  
 145 150 155 160  
 50

Val Ile Phe Trp Pro Val Pro Ala Val Leu Ala Ser Ile Gln Ile Phe  
 165 170 175

## 19

Val Phe Gly Thr Trp Leu Pro His Arg Pro Gly His Asp Asp Phe Pro  
 180 185 190

5

Asp Arg His Asn Ala Arg Ser Thr Gly Ile Gly Asp Pro Leu Ser Leu  
 195 200 205

10

Leu Thr Cys Phe His Phe Gly Gly Tyr His His Glu His His Leu His  
 210 215 220

15

Pro His Val Pro Trp Trp Arg Leu Pro Arg Thr Arg Lys Thr Gly Gly  
 225 230 235 240

Arg Ala

20

<210> 9

<211> 729

25

<212> DNA

<213> Paracoccus marcusii

30

<220>

<221> CDS

35

<222> (1)..(729)

<223>

40

<400> 9

atg agc gca cat gcc ctg ccc aag gca gat ctg acc gcc aca agc ctg  
 Met Ser Ala His Ala Leu Pro Lys Ala Asp Leu Thr Ala Thr Ser Leu

48

45

1

5

10

15

atc gtc tcg ggc ggc atc atc gcc gca tgg ctg gcc ctg cat gtg cat 96  
 Ile Val Ser Gly Gly Ile Ile Ala Ala Trp Leu Ala Leu His Val His  
 20 25 30

5

gcg ctg tgg ttt ctg gac gcg gcg gcc cat ccc atc ctg gcg gtc gcg 144  
 Ala Leu Trp Phe Leu Asp Ala Ala Ala His Pro Ile Leu Ala Val Ala  
 35 40 45

10

aat ttc ctg ggg ctg acc tgg ctg tcg gtc gga ttg ttc atc atc gcg 192  
 Asn Phe Leu Gly Leu Thr Trp Leu Ser Val Gly Leu Phe Ile Ile Ala  
 50 55 60

15

cat gac gcg atg cac ggg tcg gtc gtg ccg ggg cgt ccg cgc gcc aat 240  
 His Asp Ala Met His Gly Ser Val Val Pro Gly Arg Pro Arg Ala Asn  
 65 70 75 80

20

gcg gcg atg ggc cag ctt gtc ctg tgg ctg tat gcc gga ttt tcg tgg 288  
 Ala Ala Met Gly Gln Leu Val Leu Trp Leu Tyr Ala Gly Phe Ser Trp  
 85 90 95

25

cgc aag atg atc gtc aag cac atg gcc cat cac cgc cat gcc gga acc 336  
 Arg Lys Met Ile Val Lys His Met Ala His His Arg His Ala Gly Thr  
 100 105 110

30

gac gac gac cca gat ttc gac cat ggc ggc ccg gtc cgc tgg tac gcc 384  
 Asp Asp Asp Pro Asp Phe Asp His Gly Gly Pro Val Arg Trp Tyr Ala  
 115 120 125

35

cgc ttc atc ggc acc tat ttc ggc tgg cgc gag ggg ctg ctg ctg ccc 432  
 Arg Phe Ile Gly Thr Tyr Phe Gly Trp Arg Glu Gly Leu Leu Leu Pro  
 130 135 140

40

gtc atc gtg acg gtc tat gcg ctg atc ctg ggg gat cgc tgg atg tac 480  
 Val Ile Val Thr Val Tyr Ala Leu Ile Leu Gly Asp Arg Trp Met Tyr  
 145 150 155 160

45

gtg gtc ttc tgg ccg ttg ccg tcg atc ctg gcg tcg atc cag ctg ttc 528  
 Val Val Phe Trp Pro Leu Pro Ser Ile Leu Ala Ser Ile Gln Leu Phe  
 165 170 175

gtg ttc ggc act tgg ctg ccg cac cgc ccc ggc cac gac gcg ttc ccg 576  
 Val Phe Gly Thr Trp Leu Pro His Arg Pro Gly His Asp Ala Phe Pro  
 180 185 190



21

gac cgc cat aat gcg cgg tcg tcg cgg atc agc gac cct gtg tcg ctg 624  
 Asp Arg His Asn Ala Arg Ser Ser Arg Ile Ser Asp Pro Val Ser Leu  
 195 200 205

5 ctg acc tgc ttt cat ttt ggc ggt tat cat cac gaa cac cac ctg cac 672  
 Leu Thr Cys Phe His Phe Gly Gly Tyr His His Glu His His Leu His  
 210 215 220

10 ccg acg gtg ccg tgg tgg cgc ctg ccc agc acc cgc acc aag ggg gac 720  
 Pro Thr Val Pro Trp Trp Arg Leu Pro Ser Thr Arg Thr Lys Gly Asp  
 225 230 235 240

acc gca tga 729  
 Thr Ala

15

<210> 10

20 <211> 242  
 <212> PRT  
 <213> Paracoccus marcusii

25

<400> 10

30 Met Ser Ala His Ala Leu Pro Lys Ala Asp Leu Thr Ala Thr Ser Leu  
 1 5 10 15

Ile Val Ser Gly Gly Ile Ile Ala Ala Trp Leu Ala Leu His Val His  
 35 20 25 30

Ala Leu Trp Phe Leu Asp Ala Ala Ala His Pro Ile Leu Ala Val Ala  
 35 40 45

40

Asn Phe Leu Gly Leu Thr Trp Leu Ser Val Gly Leu Phe Ile Ile Ala  
 50 55 60

45

22

His Asp Ala Met His Gly Ser Val Val Pro Gly Arg Pro Arg Ala Asn  
 65 70 75 80

5 Ala Ala Met Gly Gln Leu Val Leu Trp Leu Tyr Ala Gly Phe Ser Trp  
 85 90 95

10 Arg Lys Met Ile Val Lys His Met Ala His His Arg His Ala Gly Thr  
 100 105 110

15 Asp Asp Asp Pro Asp Phe Asp His Gly Gly Pro Val Arg Trp Tyr Ala  
 115 120 125

Arg Phe Ile Gly Thr Tyr Phe Gly Trp Arg Glu Gly Leu Leu Leu Pro  
 130 135 140

20 Val Ile Val Thr Val Tyr Ala Leu Ile Leu Gly Asp Arg Trp Met Tyr  
 145 150 155 160

25 Val Val Phe Trp Pro Leu Pro Ser Ile Leu Ala Ser Ile Gln Leu Phe  
 165 170 175

30 Val Phe Gly Thr Trp Leu Pro His Arg Pro Gly His Asp Ala Phe Pro  
 180 185 190

35 Asp Arg His Asn Ala Arg Ser Ser Arg Ile Ser Asp Pro Val Ser Leu  
 195 200 205

40 Leu Thr Cys Phe His Phe Gly Gly Tyr His His Glu His His Leu His  
 210 215 220

45 Pro Thr Val Pro Trp Trp Arg Leu Pro Ser Thr Arg Thr Lys Gly Asp  
 225 230 235 240

45 Thr Ala

5 <210> 11  
 <211> 1629  
 <212> DNA  
 10 <213> Synechococcus sp.  
 <220>  
 15 <221> CDS  
 <222> (1)..(1629)  
 20 <223>  
 <400> 11  
 25 atg atc acc acc gat gtt gtc att att ggg gcg ggg cac aat ggc tta 48  
 Met Ile Thr Thr Asp Val Val Ile Ile Gly Ala Gly His Asn Gly Leu  
 1 5 10 15  
 gtc tgt gca gcc tat ttg ctc caa cgg ggc ttg ggg gtg acg tta cta 96  
 30 Val Cys Ala Ala Tyr Leu Leu Gln Arg Gly Leu Gly Val Thr Leu Leu  
 " 20 25 30  
 gaa aag cgg gaa gta cca ggg ggg gcg gcc acc aca gaa gct ctc atg 144  
 Glu Lys Arg Glu Val Pro Gly Gly Ala Ala Thr Thr Glu Ala Leu Met  
 35 35 40 45  
 ccg gag cta tcc ccc cag ttt cgc ttt aac cgc tgt gcc att gac cac 192  
 Pro Glu Leu Ser Pro Gln Phe Arg Phe Asn Arg Cys Ala Ile Asp His  
 50 55 60  
 40 gaa ttt atc ttt ctg ggg ccg gtg ttg cag gag cta aat tta gcc cag 240  
 Glu Phe Ile Phe Leu Gly Pro Val Leu Gln Glu Leu Asn Leu Ala Gln  
 65 70 75 80  
 45 tat ggt ttg gaa tat tta ttt tgt gac ccc agt gtt ttt tgt ccg ggg 288

	Tyr Gly Leu Glu Tyr Leu Phe Cys Asp	Pro Ser Val Phe Cys Pro Gly	
	85	90	95
5	ctg gat ggc caa gct ttt atg agc tac cgt tcc cta gaa aaa acc tgt Leu Asp Gly Gln Ala Phe Met Ser Tyr Arg Ser Leu Glu Lys Thr Cys		336
	100	105	110
10	gcc cac att gcc acc tat agc ccc cga gat gcg gaa aaa tat cgg caa Ala His Ile Ala Thr Tyr Ser Pro Arg Asp Ala Glu Lys Tyr Arg Gln		384
	115	120	125
15	ttt gtc aat tat tgg acg gat ttg ctc aac gct gtc cag cct gct ttt Phe Val Asn Tyr Trp Thr Asp Leu Leu Asn Ala Val Gln Pro Ala Phe		432
	130	135	140
	aat gct ccg ccc cag gct tta cta gat tta gcc ctg aac tat ggt tgg Asn Ala Pro Pro Gln Ala Leu Leu Asp Leu Ala Leu Asn Tyr Gly Trp		480
	145	150	155
20	gaa aac tta aaa tcc gtg ctg gcg atc gcc ggg tcg aaa acc aag gcg Glu Asn Leu Lys Ser Val Leu Ala Ile Ala Gly Ser Lys Thr Lys Ala		528
	165	170	175
25	ttg gat ttt atc cgc act atg atc ggc tcc ccg gaa gat gtg ctc aat Leu Asp Phe Ile Arg Thr Met Ile Gly Ser Pro Glu Asp Val Leu Asn		576
	180	185	190
30	gaa tgg ttc gac agc gaa cgg gtt aaa gct cct tta gct aga cta tgt Glu Trp Phe Asp Ser Glu Arg Val Lys Ala Pro Leu Ala Arg Leu Cys		624
	195	200	205
35	tcg gaa att ggc gct ccc cca tcc caa aag ggt agt agc tcc ggc atg Ser Glu Ile Gly Ala Pro Pro Ser Gln Lys Gly Ser Ser Ser Gly Met		672
	210	215	220
	atg atg gtg gcc atg cgg cat ttg gag gga att gcc aga cca aaa gga Met Met Val Ala Met Arg His Leu Glu Gly Ile Ala Arg Pro Lys Gly		720
	225	230	235
40	ggc act gga gcc ctc aca gaa gcc ttg gtg aag tta gtg caa gcc caa Gly Thr Gly Ala Leu Thr Glu Ala Leu Val Lys Leu Val Gln Ala Gln		768
	245	250	255
45	ggg gga aaa atc ctc act gac caa acc gtc aaa cgg gta ttg gtg gaa Gly Gly Lys Ile Leu Thr Asp Gln Thr Val Lys Arg Val Leu Val Glu		816

25

	260	265	270	
	aac aac cag gcg atc ggg gtg gag gta gct aac gga gaa cag tac cgg			864
	Asn Asn Gln Ala Ile Gly Val Glu Val Ala Asn Gly Glu Gln Tyr Arg			
5	275	280	285	
	gcc aaa aaa ggc gtg att tct aac atc gat gcc cgc cgt tta ttt ttg			912
	Ala Lys Lys Gly Val Ile Ser Asn Ile Asp Ala Arg Arg Leu Phe Leu			
	290	295	300	
10				
	caa ttg gtg gaa ccg ggg gcc cta gcc aag gtg aat caa aac cta ggg			960
	Gln Leu Val Glu Pro Gly Ala Leu Ala Lys Val Asn Gln Asn Leu Gly			
	305	310	315	320
15				
	gaa cga ctg gaa cgg cgc act gtg aac aat aac gaa gcc att tta aaa			1008
	Glu Arg Leu Glu Arg Arg Thr Val Asn Asn Asn Glu Ala Ile Leu Lys			
	325	330	335	
20				
	atc gat tgt gcc ctc tcc ggt tta ccc cac ttc act gcc atg gcc ggg			1056
	Ile Asp Cys Ala Leu Ser Gly Leu Pro His Phe Thr Ala Met Ala Gly			
	340	345	350	
25				
	ccg gag gat cta acg gga act att ttg att gcc gac tcg gta cgc cat			1104
	Pro Glu Asp Leu Thr Gly Thr Ile Leu Ile Ala Asp Ser Val Arg His			
	355	360	365	
30				
	gtc gag gaa gcc cac gcc ctc att gcc ttg ggg caa att ccc gat gct			1152
	Val Glu Glu Ala His Ala Leu Ile Ala Leu Gly Gln Ile Pro Asp Ala			
	370	375	380	
35				
	aat ccg tct tta tat ttg gat att ccc act gta ttg gac ccc acc atg			1200
	Asn Pro Ser Leu Tyr Leu Asp Ile Pro Thr Val Leu Asp Pro Thr Met			
	385	390	395	400
40				
	gcc ccc cct ggg cag cac acc ctc tgg atc gaa ttt ttt gcc ccc tac			1248
	Ala Pro Pro Gly Gln His Thr Leu Trp Ile Glu Phe Phe Ala Pro Tyr			
	405	410	415	
45				
	cgc atc gcc ggg ttg gaa ggg aca ggg tta atg ggc aca ggt tgg acc			1296
	Arg Ile Ala Gly Leu Glu Gly Thr Gly Leu Met Gly Thr Gly Trp Thr			
	420	425	430	
	gat gag tta aag gaa aaa gtg gcg gat cgg gtg att gat aaa tta acg			1344
	Asp Glu Leu Lys Glu Lys Val Ala Asp Arg Val Ile Asp Lys Leu Thr			
	435	440	445	

gac tat gcc cct aac cta aaa tct ctg atc att ggt cgc cga gtg gaa 1392  
 Asp Tyr Ala Pro Asn Leu Lys Ser Leu Ile Ile Gly Arg Arg Val Glu  
 450 455 460

5

agt ccc gcc gaa ctg gcc caa cgg ctg gga agt tac aac ggc aat gtc 1440  
 Ser Pro Ala Glu Leu Ala Gln Arg Leu Gly Ser Tyr Asn Gly Asn Val  
 465 470 475 480

10

tat cat ctg gat atg agt ttg gac caa atg atg ttc ctc cgg cct cta 1488  
 Tyr His Leu Asp Met Ser Leu Asp Gln Met Met Phe Leu Arg Pro Leu  
 485 490 495

15

ccg gaa att gcc aac tac caa acc ccc atc aaa aat ctt tac tta aca 1536  
 Pro Glu Ile Ala Asn Tyr Gln Thr Pro Ile Lys Asn Leu Tyr Leu Thr  
 500 505 510

20

ggg gcg ggt acc cat ccc ggt ggc tcc ata tca ggt atg ccc ggt aga 1584  
 Gly Ala Gly Thr His Pro Gly Gly Ser Ile Ser Gly Met Pro Gly Arg  
 515 520 525

25

aat tgc gct cgg gtc ttt tta aaa caa caa cgt cgt ttt tgg taa 1629  
 Asn Cys Ala Arg Val Phe Leu Lys Gln Gln Arg Arg Phe Trp  
 530 535 540

30

<210> 12  
 <211> 542  
 <212> PRT  
 <213> Synechococcus sp.

35

<400> 12

40

Met Ile Thr Thr Asp Val Val Ile Ile Gly Ala Gly His Asn Gly Leu  
 1 5 10 15

45

Val Cys Ala Ala Tyr Leu Leu Gln Arg Gly Leu Gly Val Thr Leu Leu  
 20 25 30

Glu Lys Arg Glu Val Pro Gly Gly Ala Ala Thr Thr Glu Ala Leu Met  
 35 40 45

5 Pro Glu Leu Ser Pro Gln Phe Arg Phe Asn Arg Cys Ala Ile Asp His  
 50 55 60

10 Glu Phe Ile Phe Leu Gly Pro Val Leu Gln Glu Leu Asn Leu Ala Gln  
 65 70 75 80

15 Tyr Gly Leu Glu Tyr Leu Phe Cys Asp Pro Ser Val Phe Cys Pro Gly  
 85 90 95

20 Leu Asp Gly Gln Ala Phe Met Ser Tyr Arg Ser Leu Glu Lys Thr Cys  
 100 105 110

Ala His Ile Ala Thr Tyr Ser Pro Arg Asp Ala Glu Lys Tyr Arg Gln  
 115 120 125

25 Phe Val Asn Tyr Trp Thr Asp Leu Leu Asn Ala Val Gln Pro Ala Phe  
 130 135 140

30 Asn Ala Pro Pro Gln Ala Leu Leu Asp Leu Ala Leu Asn Tyr Gly Trp  
 145 150 155 160

35 Glu Asn Leu Lys Ser Val Leu Ala Ile Ala Gly Ser Lys Thr Lys Ala  
 165 170 175

40 Leu Asp Phe Ile Arg Thr Met Ile Gly Ser Pro Glu Asp Val Leu Asn  
 180 185 190

Glu Trp Phe Asp Ser Glu Arg Val Lys Ala Pro Leu Ala Arg Leu Cys  
 195 200 205

45

## 28

Ser Glu Ile Gly Ala Pro Pro Ser Gln Lys Gly Ser Ser Ser Gly Met  
 210, 215 220

5 Met Met Val Ala Met Arg His Leu Glu Gly Ile Ala Arg Pro Lys Gly  
 225 230 235 240

10 Gly Thr Gly Ala Leu Thr Glu Ala Leu Val Lys Leu Val Gln Ala Gln  
 245 250 255

15 Gly Gly Lys Ile Leu Thr Asp Gln Thr Val Lys Arg Val Leu Val Glu  
 260 265 270

Asn Asn Gln Ala Ile Gly Val Glu Val Ala Asn Gly Glu Gln Tyr Arg  
 275 280 285

20 Ala Lys Lys Gly Val Ile Ser Asn Ile Asp Ala Arg Arg Leu Phe Leu  
 290 295 300

25 Gln Leu Val Glu Pro Gly Ala Leu Ala Lys Val Asn Gln Asn Leu Gly  
 305 310 315 320

30 Glu Arg Leu Glu Arg Arg Thr Val Asn Asn Asn Glu Ala Ile Leu Lys  
 325 330 335

35 Ile Asp Cys Ala Leu Ser Gly Leu Pro His Phe Thr Ala Met Ala Gly  
 340 345 350

Pro Glu Asp Leu Thr Gly Thr Ile Leu Ile Ala Asp Ser Val Arg His  
 355 360 365

40 Val Glu Glu Ala His Ala Leu Ile Ala Leu Gly Gln Ile Pro Asp Ala  
 370 375 380

45 Asn Pro Ser Leu Tyr Leu Asp Ile Pro Thr Val Leu Asp Pro Thr Met



385

390

395

400

Ala Pro Pro Gly Gln His Thr Leu Trp Ile Glu Phe Phe Ala Pro Tyr  
5 405 410 415

Arg Ile Ala Gly Leu Glu Gly Thr Gly Leu Met Gly Thr Gly Trp Thr  
420 425 430

Asp Glu Leu Lys Glu Lys Val Ala Asp Arg Val Ile Asp Lys Leu Thr  
435 440 445

Asp Tyr Ala Pro Asn Leu Lys Ser Leu Ile Ile Gly Arg Arg Val Glu  
450 455 460

20 Ser Pro Ala Glu Leu Ala Gln Arg Leu Gly Ser Tyr Asn Gly Asn Val  
465 470 475 480

25 Tyr His Leu Asp Met Ser Leu Asp Gln Met Met Phe Leu Arg Pro Leu  
485 490 495

Pro Glu Ile Ala Asn Tyr Gln Thr Pro Ile Lys Asn Leu Tyr Leu Thr  
500 505 510

Gly Ala Gly Thr His Pro Gly Gly Ser Ile Ser Gly Met Pro Gly Arg  
515 520 525

35  
Asn Cys Ala Arg Val Phe Leu Lys Gln Gln Arg Arg Phe Trp  
530 535 540

40       $\langle 210 \rangle$       13

<211> 776

<212> DNA

45

&lt;213&gt; Bradyrhizobium sp.

5 &lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1)..(774)

10

&lt;223&gt;

15 &lt;400&gt; 13

atg cat gca gca acc gcc aag gct act gag ttc ggg gcc tct cgg cgc 48  
 Met His Ala Ala Thr Ala Lys Ala Thr Glu Phe Gly Ala Ser Arg Arg  
 1 5 10 15

20 gac gat gcg agg cag cgc cgc gtc ggt ctc acg ctg gcc gcg gtc atc 96  
 Asp Asp Ala Arg Gln Arg Arg Val Gly Leu Thr Leu Ala Ala Val Ile  
 20 25 30

25 atc gcc gcc tgg ctg gtg ctg cat gtc ggt ctg atg ttc ttc tgg ccg 144  
 Ile Ala Ala Trp Leu Val Leu His Val Gly Leu Met Phe Phe Trp Pro  
 35 40 45

30 ctg acc ctt cac agc ctg ctg ccg gct ttg cct ctg gtg gtg ctg cag 192  
 Leu Thr Leu His Ser Leu Leu Pro Ala Leu Pro Leu Val Val Leu Gln  
 50 55 60

acc tgg ctc tat gta ggc ctg ttc atc atc gcg cat gac tgc atg cac 240  
 Thr Trp Leu Tyr Val Gly Leu Phe Ile Ile Ala His Asp Cys Met His  
 65 70 75 80

35 ggc tcg ctg gtg ccg ttc aag ccg cag gtc aac cgc cgt atc gga cag 288  
 Gly Ser Leu Val Pro Phe Lys Pro Gln Val Asn Arg Arg Ile Gly Gln  
 85 90 95

40 ctc tgc ctg ttc ctc tat gcc ggg ttc tcc ttc gac gct ctc aat gtc 336  
 Leu Cys Leu Phe Leu Tyr Ala Gly Phe Ser Phe Asp Ala Leu Asn Val  
 100 105 110

45 gag cac cac aag cat cac cgc cat ccc ggc acg gcc gag gat ccc gat 384  
 Glu His His Lys His His Arg His Pro Gly Thr Ala Glu Asp Pro Asp

	115	120	125	
	ttc gac gag gtg ccg ccg cac ggc ttc tgg cac tgg ttc gcc agc ttt			432
	Phe Asp Glu Val Pro Pro His Gly Phe Trp His Trp Phe Ala Ser Phe			
5	130	135	140	
	ttc ctg cac tat ttc ggc tgg aag cag gtc gcg atc atc gca gcc gtc			480
	Phe Leu His Tyr Phe Gly Trp Lys Gln Val Ala Ile Ile Ala Ala Val			
	145	150	155	160
10				
	tgc ctg gtt tat cag ctc gtc ttc gcc gtt ccc ttg cag aac atc ctg			528
	Ser Leu Val Tyr Gln Leu Val Phe Ala Val Pro Leu Gln Asn Ile Leu			
	165	170	175	
	ctg ttc tgg gcg ctg ccc ggg ctg ctg tgc gtc ctg tag ctg ttc acc			576
15	Leu Phe Trp Ala Leu Pro Gly Leu Leu Ser Ala Leu Gln Leu Phe Thr			
	180	185	190	
	ttc ggc acc tat ctg ccg cac aag ccg gcc acg cag ccc ttc gcc gat			624
20	Phe Gly Thr Tyr Leu Pro His Lys Pro Ala Thr Gln Pro Phe Ala Asp			
	195	200	205	
	cgc cac aac gcg cgg acg agc gaa ttt ccc gcg tgg ctg tgc ctg ctg			672
	Arg His Asn Ala Arg Thr Ser Glu Phe Pro Ala Trp Leu Ser Leu Leu			
25	210	215	220	
	acc tgc ttc cac ttc ggc ttt cat cac gag cat cat ctg cat ccc gat			720
	Thr Cys Phe His Phe Gly Phe His His Glu His His Leu His Pro Asp			
	225	230	235	240
30				
	gcg ccg tgg tgg cgg ctg ccg gag atc aag cgg cgg gcc ctg gaa agg			768
	Ala Pro Trp Trp Arg Leu Pro Glu Ile Lys Arg Arg Ala Leu Glu Arg			
	245	250	255	
35	cgt gac ta			776
	Arg Asp			
40	<210> 14			
	<211> 258			
	<212> PRT			
45				

&lt;213&gt; Bradyrhizobium sp.

5 &lt;400&gt; 14

Met His Ala Ala Thr Ala Lys Ala Thr Glu Phe Gly Ala Ser Arg Arg  
1 5 10 15

10

Asp Asp Ala Arg Gln Arg Arg Val Gly Leu Thr Leu Ala Ala Val Ile  
20 25 30

15

Ile Ala Ala Trp Leu Val Leu His Val Gly Leu Met Phe Phe Trp Pro  
35 40 45

20

Leu Thr Leu His Ser Leu Leu Pro Ala Leu Pro Leu Val Val Leu Gln  
50 55 60

25

Thr Trp Leu Tyr Val Gly Leu Phe Ile Ile Ala His Asp Cys Met His  
65 70 75 80

Gly Ser Leu Val Pro Phe Lys Pro Gln Val Asn Arg Arg Ile Gly Gln  
85 90 95

30

Leu Cys Leu Phe Leu Tyr Ala Gly Phe Ser Phe Asp Ala Leu Asn Val  
100 105 110

35

Glu His His Lys His His Arg His Pro Gly Thr Ala Glu Asp Pro Asp  
115 120 125

40

Phe Asp Glu Val Pro Pro His Gly Phe Trp His Trp Phe Ala Ser Phe  
130 135 140

45

Phe Leu His Tyr Phe Gly Trp Lys Gln Val Ala Ile Ile Ala Ala Val  
145 150 155 160

Ser Leu Val Tyr Gln Leu Val Phe Ala Val Pro Leu Gln Asn Ile Leu  
165 170 175

5 Leu Phe Trp Ala Leu Pro Gly Leu Leu Ser Ala Leu Gln Leu Phe Thr  
180 185 190

10 Phe Gly Thr Tyr Leu Pro His Lys Pro Ala Thr Gln Pro Phe Ala Asp  
195 200 205

15 Arg His Asn Ala Arg Thr Ser Glu Phe Pro Ala Trp Leu Ser Leu Leu  
210 215 220

20 Thr Cys Phe His Phe Gly Phe His His Glu His His Leu His Pro Asp  
225 230 235 240

Ala Pro Trp Trp Arg Leu Pro Glu Ile Lys Arg Arg Ala Leu Glu Arg  
245 250 255

25 Arg Asp

30 <210> 15  
<211> 777  
<212> DNA

35 <213> Nostoc sp.

40 <220>  
<221> CDS  
<222> (1)..(777)

45

&lt;223&gt;

5 <400> 15  
 atg gtt cag tgt caa cca tca tct ctg cat tca gaa aaa ctg gtg tta 48  
 Met Val Gln Cys Gln Pro Ser Ser Leu His Ser Glu Lys Leu Val Leu  
 1 5 10 15

10 ttg tca tcg aca atc aga gat gat aaa aat att aat aag ggt ata ttt 96  
 Leu Ser Ser Thr Ile Arg Asp Asp Lys Asn Ile Asn Lys Gly Ile Phe  
 20 25 30

15 att gcc tgc ttt atc tta ttt tta tgg gca att agt tta atc tta tta 144  
 Ile Ala Cys Phe Ile Leu Phe Leu Trp Ala Ile Ser Leu Ile Leu Leu  
 35 40 45

20 ctc tca ata gat aca tcc ata att cat aag agc tta tta ggt ata gcc 192  
 Leu Ser Ile Asp Thr Ser Ile Ile His Lys Ser Leu Leu Gly Ile Ala  
 50 55 60

25 atg ctt tgg cag acc ttc tta tat aca ggt tta ttt att act gct cat 240  
 Met Leu Trp Gln Thr Phe Leu Tyr Thr Gly Leu Phe Ile Thr Ala His  
 65 70 75 80

gat gcc atg cac ggc gta gtt tat ccc aaa aat ccc aga ata aat aat 288  
 Asp Ala Met His Gly Val Val Tyr Pro Lys Asn Pro Arg Ile Asn Asn  
 85 90 95

30 ttt ata ggt aag ctc act cta atc ttg tat gga cta ctc cct tat aaa 336  
 Phe Ile Gly Lys Leu Thr Leu Ile Leu Tyr Gly Leu Leu Pro Tyr Lys  
 100 105 110

35 gat tta ttg aaa aaa cat tgg tta cac cac gga cat cct ggt act gat 384  
 Asp Leu Leu Lys Lys His Trp Leu His His Gly His Pro Gly Thr Asp  
 115 120 125

40 tta gac cct gat tat tac aat ggt cat ccc caa aac ttc ttt ctt tgg 432  
 Leu Asp Pro Asp Tyr Tyr Asn Gly His Pro Gln Asn Phe Phe Leu Trp  
 130 135 140

45 tat cta cat ttt atg aag tct tat tgg cga tgg acg caa att ttc gga 480  
 Tyr Leu His Phe Met Lys Ser Tyr Trp Arg Trp Thr Gln Ile Phe Gly  
 145 150 155 160

## 35

	tta gtg atg att ttt cat gga ctt aaa aat ctg gtg cat ata cca gaa	528
	Leu Val Met Ile Phe His Gly Leu Lys Asn Leu Val His Ile Pro Glu	
	165 170 175	
5	aat aat tta att ata ttt tgg atg ata cct tct att tta agt tca gta	576
	Asn Asn Leu Ile Ile Phe Trp Met Ile Pro Ser Ile Leu Ser Ser Val	
	180 185 190	
10	caa cta ttt tat ttt ggt aca ttt ttg cct cat aaa aag cta gaa ggt	624
	Gln Leu Phe Tyr Phe Gly Thr Phe Leu Pro His Lys Lys Leu Glu Gly	
	195 200 205	
15	ggt tat act aac ccc cat tgt gcg cgc agt atc cca tta cct ctt ttt	672
	Gly Tyr Thr Asn Pro His Cys Ala Arg Ser Ile Pro Leu Pro Leu Phe	
	210 215 220	
20	tgg tct ttt gtt act tgt tat cac ttc ggc tac cac aag gaa cat cac	720
	Trp Ser Phe Val Thr Cys Tyr His Phe Gly Tyr His Lys Glu His His	
	225 230 235 240	
	gaa tac cct caa ctt cct tgg tgg aaa tta cct gaa gct cac aaa ata	768
	Glu Tyr Pro Gln Leu Pro Trp Trp Lys Leu Pro Glu Ala His Lys Ile	
	245 250 255	
25	tct tta taa	777
	Ser Leu	
30	<210> 16	
	"	
	<211> 258	
	"	
	<212> PRT	
35	<213> Nostoc sp.	
40	<400> 16	
	Met Val Gln Cys Gln Pro Ser Ser Leu His Ser Glu Lys Leu Val Leu	
	1 5 10 15	
45		

Leu Ser Ser Thr Ile Arg Asp Asp Lys Asn Ile Asn Lys Gly Ile Phe  
 20 25 30

5 Ile Ala Cys Phe Ile Leu Phe Leu Trp Ala Ile Ser Leu Ile Leu Leu  
 35 40 45

10 Leu Ser Ile Asp Thr Ser Ile Ile His Lys Ser Leu Leu Gly Ile Ala  
 50 55 60

15 Met Leu Trp Gln Thr Phe Leu Tyr Thr Gly Leu Phe Ile Thr Ala His  
 65 70 75 80

20 Asp Ala Met His Gly Val Val Tyr Pro Lys Asn Pro Arg Ile Asn Asn  
 85 90 95

Phe Ile Gly Lys Leu Thr Leu Ile Leu Tyr Gly Leu Leu Pro Tyr Lys  
 100 105 110

25 Asp Leu Leu Lys Lys His Trp Leu His His Gly His Pro Gly Thr Asp  
 115 120 125

30 Leu Asp Pro Asp Tyr Tyr Asn Gly His Pro Gln Asn Phe Phe Leu Trp  
 130 135 140

35 Tyr Leu His Phe Met Lys Ser Tyr Trp Arg Trp Thr Gln Ile Phe Gly  
 145 150 155 160

Leu Val Met Ile Phe His Gly Leu Lys Asn Leu Val His Ile Pro Glu  
 165 170 175

40 Asn Asn Leu Ile Ile Phe Trp Met Ile Pro Ser Ile Leu Ser Ser Val  
 180 185 190

45 Gln Leu Phe Tyr Phe Gly Thr Phe Leu Pro His Lys Lys Leu Glu Gly



195

200

205

5 Gly Tyr Thr Asn Pro His Cys Ala Arg Ser Ile Pro Leu Pro Leu Phe  
210 215 220

10 Trp Ser Phe Val Thr Cys Tyr His Phe Gly Tyr His Lys Glu His His  
225 230 235 240

15 Glu Tyr Pro Gln Leu Pro Trp Trp Lys Leu Pro Glu Ala His Lys Ile  
245 250 255  
Ser Leu

20 <210> 17  
<211> 1608

25 <212> DNA  
<213> Haematococcus pluvialis

30 <220>  
" <221> CDS  
<222> (3)..(971)  
35 <223>

40 <400> 17  
ct aca ttt cac aag ccc gtg agc ggt gca agc gct ctg ccc cac atc 47  
Thr Phe His Lys Pro Val Ser Gly Ala Ser Ala Leu Pro His Ile  
1 5 10 15

45 ggc cca cct cct cat ctc cat cgg tca ttt gct gct acc acg atg ctg 95

38

	Gly	Pro	Pro	Pro	His	Leu	His	Arg	Ser	Phe	Ala	Ala	Thr	Thr	Met	Leu	
					20					25					30		
	tcg	aag	ctg	cag	tca	atc	agc	gtc	aag	gcc	cgc	cgc	gtt	gaa	cta	gcc	143
5	Ser	Lys	Leu	Gln	Ser	Ile	Ser	Val	Lys	Ala	Arg	Arg	Val	Glu	Leu	Ala	
				35					40					45			
	cgc	gac	atc	acg	cgg	ccc	aaa	gtc	tgc	ctg	cat	gct	cag	cgg	tgc	tcg	191
10	Arg	Asp	Ile	Thr	Arg	Pro	Lys	Val	Cys	Leu	His	Ala	Gln	Arg	Cys	Ser	
			50					55					60				
	tta	gtt	cgg	ctg	cga	gtg	gca	gca	cca	cag	aca	gag	gag	gcg	ctg	gga	239
	Leu	Val	Arg	Leu	Arg	Val	Ala	Ala	Pro	Gln	Thr	Glu	Glu	Ala	Leu	Gly	
		65					70					75					
15	acc	gtg	cag	gct	gcc	ggc	gcg	ggc	gat	gag	cac	agc	gcc	gat	gta	gca	287
	Thr	Val	Gln	Ala	Ala	Gly	Ala	Gly	Asp	Glu	His	Ser	Ala	Asp	Val	Ala	
	80					85				90					95		
20	ctc	cag	cag	ctt	gac	cgg	gct	atc	gca	gag	cgt	cgt	gcc	cgg	cgc	aaa	335
	Leu	Gln	Gln	Leu	Asp	Arg	Ala	Ile	Ala	Glu	Arg	Arg	Ala	Arg	Arg	Lys	
					100					105					110		
	cgg	gag	cag	ctg	tca	tac	cag	gct	gcc	gcc	att	gca	gca	tca	att	ggc	383
25	Arg	Glu	Gln	Leu	Ser	Tyr	Gln	Ala	Ala	Ala	Ile	Ala	Ala	Ser	Ile	Gly	
				115					120					125			
	gtg	tca	ggc	att	gcc	atc	ttc	gcc	acc	tac	ctg	aga	ttt	gcc	atg	cac	431
30	Val	Ser	Gly	Ile	Ala	Ile	Phe	Ala	Thr	Tyr	Leu	Arg	Phe	Ala	Met	His	
			130					135					140				
	atg	acc	gtg	ggc	ggc	gca	gtg	cca	tgg	ggt	gaa	gtg	gct	ggc	act	ctc	479
	Met	Thr	Val	Gly	Gly	Ala	Val	Pro	Trp	Gly	Glu	Val	Ala	Gly	Thr	Leu	
		145					150				155						
35	ctc	ttg	gtg	gtt	ggt	ggc	gcg	ctc	ggc	atg	gag	atg	tat	gcc	cgc	tat	527
	Leu	Leu	Val	Val	Gly	Gly	Ala	Leu	Gly	Met	Glu	Met	Tyr	Ala	Arg	Tyr	
	160					165					170				175		
40	gca	cac	aaa	gcc	atc	tgg	cat	gag	tcg	cct	ctg	ggc	tgg	ctg	ctg	cac	575
	Ala	His	Lys	Ala	Ile	Trp	His	Glu	Ser	Pro	Leu	Gly	Trp	Leu	Leu	His	
					180					185				190			
	aag	agc	cac	cac	aca	cct	cgc	act	gga	ccc	ttt	gaa	gcc	aac	gac	ttg	623
45	Lys	Ser	His	His	Thr	Pro	Arg	Thr	Gly	Pro	Phe	Glu	Ala	Asn	Asp	Leu	

	195	200	205	
	ttt gca atc atc aat gga ctg ccc gcc atg ctc ctg tgt acc ttt ggc			671
	Phe Ala Ile Ile Asn Gly Leu Pro Ala Met Leu Leu Cys Thr Phe Gly			
5	210	215	220	
	ttc tgg ctg ccc aac gtc ctg ggg gcg gcc tgc ttt gga gcg ggg ctg			719
	Phe Trp Leu Pro Asn Val Leu Gly Ala Ala Cys Phe Gly Ala Gly Leu			
	225	230	235	
10	ggc atc acg cta tac ggc atg gca tat atg ttt gta cac gat ggc ctg			767
	Gly Ile Thr Leu Tyr Gly Met Ala Tyr Met Phe Val His Asp Gly Leu			
	240	245	250	255
15	gtg cac agg cgc ttt ccc acc ggg ccc atc gct ggc ctg ccc tac atg			815
	Val His Arg Arg Phe Pro Thr Gly Pro Ile Ala Gly Leu Pro Tyr Met			
	260	265	270	
	aag cgc ctg aca gtg gcc cac cag cta cac cac agc ggc aag tac ggt			863
20	Lys Arg Leu Thr Val Ala His Gln Leu His His Ser Gly Lys Tyr Gly			
	275	280	285	
	ggc gcg ccc tgg ggt atg ttc ttg ggt cca cag gag ctg cag cac att			911
	Gly Ala Pro Trp Gly Met Phe Leu Gly Pro Gln Glu Leu Gln His Ile			
25	290	295	300	
	cca ggt gcg gcg gag gag gtg gag cga ctg gtc ctg gaa ctg gac tgg			959
	Pro Gly Ala Ala Glu Glu Val Glu Arg Leu Val Leu Glu Leu Asp Trp			
	305	310	315	
30	tcc aag cgg tag ggtgcggaac caggcacgct gggttcacac ctcatgcctg			1011
	Ser Lys Arg			
	320			
35	tgataaggtg tggctagagc gatgcgtgtg agacgggtat gtcacgggtcg actggtctga			1071
	tggccaatgg catcgcccat gtctggtcat cacgggctgg ttgcctgggt gaaggtgatg			1131
	cacatcatca tgtgcggttg gaggggctgg cacagtgtgg gctgaactgg agcagttgtc			1191
40	caggctggcg ttgaatcagt gagggtttgt gattggcggg tgtgaagcaa tgactccgcc			1251
	catattctat ttgtgggagc tgagatgatg gcatgcttgg gatgtgcatg gatcatggta			1311
45	gtgcagcaaa ctatattcac ctagggtgtg tggtaggatc aggtgaggcc ttgcacattg			1371

catgatgtac tcgtcatggt gtgttggtga gaggatggat gtggatggat gtgtattctc 1431  
 agacgtagac cttgactgga ggcttgatcg agagagtggg ccgtattctt tgagagggga 1491  
 5 ggctcgtgcc agaaatggtg agtggatgac tgtgacgctg tacattgcag gcagggtgaga 1551  
 tgcactgtct cgattgtaaa atacattcag atgcaaaaaa aaaaaaaaaa aaaaaaa 1608  
 10  
 <210> 18  
 <211> 322  
 15 <212> PRT  
 <213> Haematococcus pluvialis  
 20  
 <400> 18  
 Thr Phe His Lys Pro Val Ser Gly Ala Ser Ala Leu Pro His Ile Gly  
 1 5 10 15  
 25 Pro Pro Pro His Leu His Arg Ser Phe Ala Ala Thr Thr Met Leu Ser  
 20 25 30  
 30 Lys Leu Gln Ser Ile Ser Val Lys Ala Arg Arg Val Glu Leu Ala Arg  
 35 40 45  
 35 Asp Ile Thr Arg Pro Lys Val Cys Leu His Ala Gln Arg Cys Ser Leu  
 50 55 60  
 Val Arg Leu Arg Val Ala Ala Pro Gln Thr Glu Glu Ala Leu Gly Thr  
 40 65 70 75 80  
 Val Gln Ala Ala Gly Ala Gly Asp Glu His Ser Ala Asp Val Ala Leu  
 85 90 95  
 45

Gln Gln Leu Asp Arg Ala Ile Ala Glu Arg Arg Ala Arg Arg Lys Arg  
 100 105 110

5

Glu Gln Leu Ser Tyr Gln Ala Ala Ala Ile Ala Ala Ser Ile Gly Val  
 115 120 125

10

Ser Gly Ile Ala Ile Phe Ala Thr Tyr Leu Arg Phe Ala Met His Met  
 130 135 140

15

Thr Val Gly Gly Ala Val Pro Trp Gly Glu Val Ala Gly Thr Leu Leu  
 145 150 155 160

20

Leu Val Val Gly Gly Ala Leu Gly Met Glu Met Tyr Ala Arg Tyr Ala  
 165 170 175

25

His Lys Ala Ile Trp His Glu Ser Pro Leu Gly Trp Leu Leu His Lys  
 180 185 190

Ser His His Thr Pro Arg Thr Gly Pro Phe Glu Ala Asn Asp Leu Phe  
 195 200 205

30

Ala Ile Ile Asn Gly Leu Pro Ala Met Leu Leu Cys Thr Phe Gly Phe  
 210 215 220

35

Trp Leu Pro Asn Val Leu Gly Ala Ala Cys Phe Gly Ala Gly Leu Gly  
 225 230 235 240

40

Ile Thr Leu Tyr Gly Met Ala Tyr Met Phe Val His Asp Gly Leu Val  
 245 250 255

His Arg Arg Phe Pro Thr Gly Pro Ile Ala Gly Leu Pro Tyr Met Lys  
 260 265 270

45

42

Arg Leu Thr Val Ala His Gln Leu His His Ser Gly Lys Tyr Gly Gly  
 275 280 285

5 Ala Pro Trp Gly Met Phe Leu Gly Pro Gln Glu Leu Gln His Ile Pro  
 290 295 300

10 Gly Ala Ala Glu Glu Val Glu Arg Leu Val Leu Glu Leu Asp Trp Ser  
 305 310 315 320

Lys Arg

15

<210> 19

<211> 1503

20

<212> DNA

<213> Tomato

25

<220>

<221> CDS

30

<222> (1) .. (1503)

<223>

35

<400> 19

atg gat act ttg ttg aaa acc cca aat aac ctt gaa ttt ctg aac cca 48

Met Asp Thr Leu Leu Lys Thr Pro Asn Asn Leu Glu Phe Leu Asn Pro

40

1 5 10 15

cat cat ggt ttt gct gtt aaa gct agt acc ttt aga tct gag aag cat 96

His His Gly Phe Ala Val Lys Ala Ser Thr Phe Arg Ser Glu Lys His

20

25

30

45

	cat aat ttt ggt tct agg aag ttt tgt gaa act ttg ggt aga agt gtt	144
	His Asn, Phe Gly Ser Arg Lys Phe Cys Glu Thr Leu Gly Arg Ser Val	
	35 40 45	
5	tgt gtt aag ggt agt agt agt gct ctt tta gag ctt gta cct gag acc	192
	Cys Val Lys Gly Ser Ser Ser Ala Leu Leu Glu Leu Val Pro Glu Thr	
	50 55 60	
10	aaa aag gag aat ctt gat ttt gag ctt cct atg tat gac cct tca aaa	240
	Lys Lys Glu Asn Leu Asp Phe Glu Leu Pro Met Tyr Asp Pro Ser Lys	
	65 70 75 80	
15	ggg gtt gtt gtg gat ctt gct gtg gtt ggt ggt ggc cct gca gga ctt	288
	Gly Val Val Val Asp Leu Ala Val Val Gly Gly Gly Pro Ala Gly Leu	
	85 90 95	
20	gct gtt gca cag caa gtt tct gaa gca gga ctc tct gtt tgt tca att	336
	Ala Val Ala Gln Gln Val Ser Glu Ala Gly Leu Ser Val Cys Ser Ile	
	100 105 110	
25	gat ccg aat cct aaa ttg ata tgg cct aat aac tat ggt gtt tgg gtg	384
	Asp Pro Asn Pro Lys Leu Ile Trp Pro Asn Asn Tyr Gly Val Trp Val	
	115 120 125	
30	gat gaa ttt gag gct atg gac ttg tta gat tgt cta gat gct acc tgg	432
	Asp Glu Phe Glu Ala Met Asp Leu Leu Asp Cys Leu Asp Ala Thr Trp	
	130 135 140	
35	tct ggt gca gca gtg tac att gat gat aat acg gct aaa gat ctt cat	480
	Ser Gly Ala Ala Val Tyr Ile Asp Asp Asn Thr Ala Lys Asp Leu His	
	145 150 155 160	
40	aga cct tat gga agg gtt aac cgg aaa cag ctg aaa tcg aaa atg atg	528
	Arg Pro Tyr Gly Arg Val Asn Arg Lys Gln Leu Lys Ser Lys Met Met	
	165 170 175	
45	cag aaa tgt ata atg aat ggt gtt aaa ttc cac caa gcc aaa gtt ata	576
	Gln Lys Cys Ile Met Asn Gly Val Lys Phe His Gln Ala Lys Val Ile	
	180 185 190	
50	aag gtg att cat gag gaa tcg aaa tcc atg ttg ata tgc aat gat ggt	624
	Lys Val Ile His Glu Glu Ser Lys Ser Met Leu Ile Cys Asn Asp Gly	
	195 200 205	
55	att act att cag gca acg gtg gtg ctc gat gca act ggc ttc tct aga	672

	Ile Thr Ile Gln Ala Thr Val Val Leu Asp Ala Thr Gly Phe Ser Arg	
	210 215 220	
5	tct ctt gtt cag tat gat aag cct tat aac ccc ggg tat caa gtt gct Ser Leu Val Gln Tyr Asp Lys Pro Tyr Asn Pro Gly Tyr Gln Val Ala	720
	225 230 235 240	
10	tat ggc att ttg gct gaa gtg gaa gag cac ccc ttt gat gta aac aag Tyr Gly Ile Leu Ala Glu Val Glu Glu His Pro Phe Asp Val Asn Lys	768
	245 250 255	
15	atg gtt ttc atg gat tgg cga gat tct cat ttg aag aac aat act gat Met Val Phe Met Asp Trp Arg Asp Ser His Leu Lys Asn Asn Thr Asp	816
	260 265 270	
20	ctc aag gag aga aat agt aga ata cca act ttt ctt tat gca atg cca Leu Lys Glu Arg Asn Ser Arg Ile Pro Thr Phe Leu Tyr Ala Met Pro	864
	275 280 285	
25	ttt tca tcc aac agg ata ttt ctt gaa gaa aca tca ctc gta gct cgt Phe Ser Ser Asn Arg Ile Phe Leu Glu Glu Thr Ser Leu Val Ala Arg	912
	290 295 300	
30	cct ggc ttg cgt ata gat gat att caa gaa cga atg gtg gct cgt tta Pro Gly Leu Arg Ile Asp Asp Ile Gln Glu Arg Met Val Ala Arg Leu	960
	305 310 315 320	
35	aac cat ttg ggg ata aaa gtg aag agc att gaa gaa gat gaa cat tgt Asn His Leu Gly Ile Lys Val Lys Ser Ile Glu Glu Asp Glu His Cys	1008
	325 330 335	
40	cta ata cca atg ggt ggt cca ctt cca gta tta cct cag aga gtc gtt Leu Ile Pro Met Gly Gly Pro Leu Pro Val Leu Pro Gln Arg Val Val	1056
	340 345 350	
45	gga atc ggt ggt aca gct ggc atg gtt cat cca tcc acc ggt tat atg Gly Ile Gly Gly Thr Ala Gly Met Val His Pro Ser Thr Gly Tyr Met	1104
	355 360 365	
50	gtg gca agg aca cta gct gcg gct cct gtt gtt gcc aat gcc ata att Val Ala Arg Thr Leu Ala Ala Ala Pro Val Val Ala Asn Ala Ile Ile	1152
	370 375 380	
55	caa tac ctc ggt tct gaa aga agt cat tcg ggt aat gaa tta tcc aca Gln Tyr Leu Gly Ser Glu Arg Ser His Ser Gly Asn Glu Leu Ser Thr	1200



45

	385		390		395		400	
	gct gtt tgg aaa gat ttg tgg cct ata gag agg aga cgt caa aga gag							1248
	Ala Val Trp Lys Asp Leu Trp Pro Ile Glu Arg Arg Arg Gln Arg Glu							
5			405		410		415	
	ttc ttc tgc ttc ggt atg gat att ctt ctg aag ctt gat tta cct gct							1296
	Phe Phe Cys Phe Gly Met Asp Ile Leu Leu Lys Leu Asp Leu Pro Ala							
			420		425		430	
10	aca aga agg ttc ttt gat gca ttc ttt gac tta gaa cct cgt tat tgg							1344
	Thr Arg Arg Phe Phe Asp Ala Phe Phe Asp Leu Glu Pro Arg Tyr Trp							
			435		440		445	
15	cat ggc ttc tta tcg tct cga ttg ttt cta cct gaa ctc ata gtt ttt							1392
	His Gly Phe Leu Ser Ser Arg Leu Phe Leu Pro Glu Leu Ile Val Phe							
			450		455		460	
	ggg ctg tct cta ttc tct cat gct tca aat act tct aga ttt gag ata							1440
20	Gly Leu Ser Leu Phe Ser His Ala Ser Asn Thr Ser Arg Phe Glu Ile							
			465		470		475	480
	atg aca aag gga act gtt cca tta gta aat atg atc aac aat ttg tta							1488
	Met Thr Lys Gly Thr Val Pro Leu Val Asn Met Ile Asn Asn Leu Leu							
25			485		490		495	
	cag gat aaa gaa tga							1503
	Gln Asp Lys Glu							
			500					
30								
	<210> 20							
	<211> 500							
35	<212> PRT							
	<213> Tomato							
40								
	<400> 20							
	Met Asp Thr Leu Leu Lys Thr Pro Asn Asn Leu Glu Phe Leu Asn Pro							
45	1		5		10		15	

His His Gly Phe Ala Val Lys Ala Ser Thr Phe Arg Ser Glu Lys His  
 20 25 30  
 5

His Asn Phe Gly Ser Arg Lys Phe Cys Glu Thr Leu Gly Arg Ser Val  
 35 40 45  
 10

Cys Val Lys Gly Ser Ser Ser Ala Leu Leu Glu Leu Val Pro Glu Thr  
 50 55 60  
 15

Lys Lys Glu Asn Leu Asp Phe Glu Leu Pro Met Tyr Asp Pro Ser Lys  
 65 70 75 80  
 20

Gly Val Val Val Asp Leu Ala Val Val Gly Gly Gly Pro Ala Gly Leu  
 85 90 95  
 25

Ala Val Ala Gln Gln Val Ser Glu Ala Gly Leu Ser Val Cys Ser Ile  
 100 105 110  
 30

Asp Pro Asn Pro Lys Leu Ile Trp Pro Asn Asn Tyr Gly Val Trp Val  
 115 120 125  
 35

Asp Glu Phe Glu Ala Met Asp Leu Leu Asp Cys Leu Asp Ala Thr Trp  
 130 135 140  
 40

Ser Gly Ala Ala Val Tyr Ile Asp Asp Asn Thr Ala Lys Asp Leu His  
 145 150 155 160  
 45

Arg Pro Tyr Gly Arg Val Asn Arg Lys Gln Leu Lys Ser Lys Met Met  
 165 170 175  
 50

Gln Lys Cys Ile Met Asn Gly Val Lys Phe His Gln Ala Lys Val Ile  
 180 185 190  
 55

Lys Val Ile His Glu Glu Ser Lys Ser Met Leu Ile Cys Asn Asp Gly  
 195 200 205

5

Ile Thr Ile Gln Ala Thr Val Val Leu Asp Ala Thr Gly Phe Ser Arg  
 210 215 220

10

Ser Leu Val Gln Tyr Asp Lys Pro Tyr Asn Pro Gly Tyr Gln Val Ala  
 225 230 235 240

15

Tyr Gly Ile Leu Ala Glu Val Glu Glu His Pro Phe Asp Val Asn Lys  
 245 250 255

20

Met Val Phe Met Asp Trp Arg Asp Ser His Leu Lys Asn Asn Thr Asp  
 260 265 270

Leu Lys Glu Arg Asn Ser Arg Ile Pro Thr Phe Leu Tyr Ala Met Pro  
 275 280 285

25

Phe Ser Ser Asn Arg Ile Phe Leu Glu Glu Thr Ser Leu Val Ala Arg  
 290 295 300

30

Pro Gly Leu Arg Ile Asp Asp Ile Gln Glu Arg Met Val Ala Arg Leu  
 305 310 315 320

35

Asn His Leu Gly Ile Lys Val Lys Ser Ile Glu Glu Asp Glu His Cys  
 325 330 335

40

Leu Ile Pro Met Gly Gly Pro Leu Pro Val Leu Pro Gln Arg Val Val  
 340 345 350

Gly Ile Gly Gly Thr Ala Gly Met Val His Pro Ser Thr Gly Tyr Met  
 355 360 365

45

Val Ala Arg Thr Leu Ala Ala Ala Pro Val Val Ala Asn Ala Ile Ile  
 370 375 380

5 Gln Tyr Leu Gly Ser Glu Arg Ser His Ser Gly Asn Glu Leu Ser Thr  
 385 390 395 400

10 Ala Val Trp Lys Asp Leu Trp Pro Ile Glu Arg Arg Arg Gln Arg Glu  
 405 410 415

15 Phe Phe Cys Phe Gly Met Asp Ile Leu Leu Lys Leu Asp Leu Pro Ala  
 420 425 430

Thr Arg Arg Phe Phe Asp Ala Phe Phe Asp Leu Glu Pro Arg Tyr Trp  
 435 440 445

20 His Gly Phe Leu Ser Ser Arg Leu Phe Leu Pro Glu Leu Ile Val Phe  
 450 455 460

25 Gly Leu Ser Leu Phe Ser His Ala Ser Asn Thr Ser Arg Phe Glu Ile  
 465 470 475 480

30 Met Thr Lys Gly Thr Val Pro Leu Val Asn Met Ile Asn Asn Leu Leu  
 485 490 495

Gln Asp Lys Glu  
 500

35

&lt;210&gt; 21

&lt;211&gt; 195

40

&lt;212&gt; DNA

&lt;213&gt; Potato

<220>

5 <221> Intron

<222> (1)..(195)

<223>

10

<400> 21

15 tacgtaagtt tctgcttcta cctttgatat atatataata attatcatta attagtagta 60

atataatatt tcaaataattt ttttcaaaat aaaagaatgt agtatatagc aattgctttt 120

ctgtagttta taagtgtgta tattttaatt tataactttt ctaatatatg accaaaattt 180

20 gttgatgtgc agctg 195

<210> 22

25 <211> 1155

<212> DNA

<213> Haematococcus pluvialis

30

<220>

35 <221> CDS

<222> (6)..(995)

<223>

40

<400> 22

45 gaagc atg cag cta gca gcg aca gta atg ttg gag cag ctt acc gga agc 50

Met Gln Leu Ala Ala Thr Val Met Leu Glu Gln Leu Thr Gly Ser

50

	1	5	10	15	
	gct gag gca ctc aag gag aag gag aag gag gtt gca ggc agc tct gac				98
	Ala Glu Ala Leu Lys Glu Lys Glu Lys Glu Val Ala Gly Ser Ser Asp				
5		20	25	30	
	gtg ttg cgt aca tgg gcg acc cag tac tcg ctt ccg tca gag gag tca				146
	Val Leu Arg Thr Trp Ala Thr Gln Tyr Ser Leu Pro Ser Glu Glu Ser				
		35	40	45	
10					
	gac gcg gcc cgc ccg gga ctg aag aat gcc tac aag cca cca cct tcc				194
	Asp Ala Ala Arg Pro Gly Leu Lys Asn Ala Tyr Lys Pro Pro Pro Ser				
		50	55	60	
15					
	gac aca aag ggc atc aca atg gcg cta gct gtc atc ggc tcc tgg gcc				242
	Asp Thr Lys Gly Ile Thr Met Ala Leu Ala Val Ile Gly Ser Trp Ala				
		65	70	75	
	gca gtg ttc ctc cac gcc att ttt caa atc aag ctt ccg acc tcc ttg				290
20	Ala Val Phe Leu His Ala Ile Phe Gln Ile Lys Leu Pro Thr Ser Leu				
		80	85	90	95
	gac cag ctg cac tgg ctg ccc gtg tca gat gcc aca gct cag ctg gtt				338
	Asp Gln Leu His Trp Leu Pro Val Ser Asp Ala Thr Ala Gln Leu Val				
25		100	105	110	
	agc ggc agc agc agc ctg ctg cac atc gtc gta gta ttc ttt gtc ctg				386
	Ser Gly Ser Ser Ser Leu Leu His Ile Val Val Val Phe Phe Val Leu				
		115	120	125	
30					
	gag ttc ctg tac aca ggc ctt ttt atc acc acg cat gat gct atg cat				434
	Glu Phe Leu Tyr Thr Gly Leu Phe Ile Thr Thr His Asp Ala Met His				
		130	135	140	
35					
	ggc acc atc gcc atg aga aac agg cag ctt aat gac ttc ttg ggc aga				482
	Gly Thr Ile Ala Met Arg Asn Arg Gln Leu Asn Asp Phe Leu Gly Arg				
		145	150	155	
	gta tgc atc tcc ttg tac gcc tgg ttt gat tac aac atg ctg cac cgc				530
40	Val Cys Ile Ser Leu Tyr Ala Trp Phe Asp Tyr Asn Met Leu His Arg				
		160	165	170	175
	aag cat tgg gag cac cac aac cac act ggc gag gtg ggc aag gac cct				578
	Lys His Trp Glu His His Asn His Thr Gly Glu Val Gly Lys Asp Pro				
45		180	185	190	

	gac ttc,cac agg gga aac cct ggc att gtg ccc tgg ttt gcc agc ttc	626
	Asp Phe His Arg Gly Asn Pro Gly Ile Val Pro Trp Phe Ala Ser Phe	
	195 200 205	
5		
	atg tcc agc tac atg tcg atg tgg cag ttt gcg cgc ctc gca tgg tgg	674
	Met Ser Ser Tyr Met Ser Met Trp Gln Phe Ala Arg Leu Ala Trp Trp	
	210 215 220	
10		
	acg gtg gtc atg cag ctg ctg ggt gcg cca atg gcg aac ctg ctg gtg	722
	Thr Val Val Met Gln Leu Leu Gly Ala Pro Met Ala Asn Leu Leu Val	
	225 230 235	
	ttc atg gcg gcc gcg ccc atc ctg tcc gcc ttc cgc ttg ttc tac ttt	770
15	Phe Met Ala Ala Ala Pro Ile Leu Ser Ala Phe Arg Leu Phe Tyr Phe	
	240 245 250 255	
	ggc acg tac atg ccc cac aag cct gag cct ggc gcc gcg tca ggc tct	818
	Gly Thr Tyr Met Pro His Lys Pro Glu Pro Gly Ala Ala Ser Gly Ser	
20	260 265 270	
	tca cca gcc gtc atg aac tgg tgg aag tcg cgc act agc cag gcg tcc	866
	Ser Pro Ala Val Met Asn Trp Trp Lys Ser Arg Thr Ser Gln Ala Ser	
	275 280 285	
25		
	gac ctg gtc agc ttt ctg acc tgc tac cac ttc gac ctg cac tgg gag	914
	Asp Leu Val Ser Phe Leu Thr Cys Tyr His Phe Asp Leu His Trp Glu	
	290 295 300	
30		
	cac cac cgc tgg ccc ttt gcc ccc tgg tgg gag ctg ccc aac tgc cgc	962
	His His Arg Trp Pro Phe Ala Pro Trp Trp Glu Leu Pro Asn Cys Arg	
	305 310 315	
	cgc ctg tct ggc cga ggt ctg gtt cct gcc tag ctggacacac tgcagtgggc	1015
35	Arg Leu Ser Gly Arg Gly Leu Val Pro Ala	
	320 325	
	cctgctgccca gctgggcatg cagggttgagg caggactggg tgagggtgaaa agctgcaggc	1075
40		
	gctgctgccg gacacgctgc atgggctacc ctgtgtagct gccgccacta ggggaggggg	1135
	tttgtagctg tcgagcttgc	1155

&lt;210&gt; 23

&lt;211&gt; 329

5 &lt;212&gt; PRT

&lt;213&gt; Haematococcus pluvialis

10

&lt;400&gt; 23

Met Gln Leu Ala Ala Thr Val Met Leu Glu Gln Leu Thr Gly Ser Ala  
 1 5 10 15

15

Glu Ala Leu Lys Glu Lys Glu Lys Glu Val Ala Gly Ser Ser Asp Val  
 20 25 30

20

Leu Arg Thr Trp Ala Thr Gln Tyr Ser Leu Pro Ser Glu Glu Ser Asp  
 35 40 45

25

Ala Ala Arg Pro Gly Leu Lys Asn Ala Tyr Lys Pro Pro Pro Ser Asp  
 50 55 60

30

Thr Lys Gly Ile Thr Met Ala Leu Ala Val Ile Gly Ser Trp Ala Ala  
 65 70 75 80

35

Val Phe Leu His Ala Ile Phe Gln Ile Lys Leu Pro Thr Ser Leu Asp  
 85 90 95

40

Gln Leu His Trp Leu Pro Val Ser Asp Ala Thr Ala Gln Leu Val Ser  
 100 105 110

Gly Ser Ser Ser Leu Leu His Ile Val Val Val Phe Phe Val Leu Glu  
 115 120 125

45

Phe Leu Tyr Thr Gly Leu Phe Ile Thr Thr His Asp Ala Met His Gly



130

135

140

5 Thr Ile Ala Met Arg Asn Arg Gln Leu Asn Asp Phe Leu Gly Arg Val  
145 150 155 160

10 Cys Ile Ser Leu Tyr Ala Trp Phe Asp Tyr Asn Met Leu His Arg Lys  
165 170 175

His Trp Glu His His Asn His Thr Gly Glu Val Gly Lys Asp Pro Asp  
180 185 190

15 Phe His Arg Gly Asn Pro Gly Ile Val Pro Trp Phe Ala Ser Phe Met  
195 200 205

20 Ser Ser Tyr Met Ser Met Trp Gln Phe Ala Arg Leu Ala Trp Trp Thr  
210 215 220

25 Val Val Met Gln Leu Leu Gly Ala Pro Met Ala Asn Leu Leu Val Phe  
225 230 235 240

30 Met Ala Ala Ala Pro Ile Leu Ser Ala Phe Arg Leu Phe Tyr Phe Gly  
245 250 255

Thr Tyr Met Pro His Lys Pro Glu Pro Gly Ala Ala Ser Gly Ser Ser  
260 265 270

35 Pro Ala Val Met Asn Trp Trp Lys Ser Arg Thr Ser Gln Ala Ser Asp  
275 280 285

40 Leu Val Ser Phe Leu Thr Cys Tyr His Phe Asp Leu His Trp Glu His  
290 295 300

45 His Arg Trp Pro Phe Ala Pro Trp Trp Glu Leu Pro Asn Cys Arg Arg  
305 310 315 320

Leu Ser Gly Arg Gly Leu Val Pro Ala

325

5

<210> 24

<211> 1111

10

<212> DNA

<213> Haematococcus pluvialis

15

<220>

<221> CDS

20

<222> (4)...(951),

<223>

25

<400> 24

tgc atg cta gag gca ctc aag gag aag gag aag gag gtt gca ggc agc 48

Met Leu Glu Ala Leu Lys Glu Lys Glu Lys Glu Val Ala Gly Ser

30

1

5

10

15

tct gac gtg ttg cgt aca tgg gcg acc cag tac tcg ctt ccg tca gaa 96

Ser Asp Val Leu Arg Thr Trp Ala Thr Gln Tyr Ser Leu Pro Ser Glu

20

25

30

35

gag tca gac gcg gcc cgc ccg gga ctg aag aat gcc tac aag cca cca 144

Glu Ser Asp Ala Ala Arg Pro Gly Leu Lys Asn Ala Tyr Lys Pro Pro

35

40

45

40

cct tcc gac aca aag ggc atc aca atg gcg cta gct gtc atc ggc tcc 192

Pro Ser Asp Thr Lys Gly Ile Thr Met Ala Leu Ala Val Ile Gly Ser

50

55

60

tgg gcc gca gtg ttc ctc cac gcc att ttt caa atc aag ctt ccg acc 240

45

Trp Ala Ala Val Phe Leu His Ala Ile Phe Gln Ile Lys Leu Pro Thr

	65	70	75	
	tcc ttg gac cag ctg cac tgg ctg ccc gtg tca gat gcc aca gct cag			288
	Ser Leu Asp Gln Leu His Trp Leu Pro Val Ser Asp Ala Thr Ala Gln			
5	80	85	90	95
	ctg gtt agc ggc agc agc agc ctg ctg cac atc gtc gta gta ttc ttt			336
	Leu Val Ser Gly Ser Ser Ser Leu Leu His Ile Val Val Val Phe Phe			
	100	105	110	
10	gtc ctg gag ttc ctg tac aca ggc ctt ttt atc acc acg cat gat gct			384
	Val Leu Glu Phe Leu Tyr Thr Gly Leu Phe Ile Thr Thr His Asp Ala			
	115	120	125	
15	atg cat ggc acc atc gcc atg aga aac agg cag ctt aat gac ttc ttg			432
	Met His Gly Thr Ile Ala Met Arg Asn Arg Gln Leu Asn Asp Phe Leu			
	130	135	140	
	ggc aga gta tgc atc tcc ttg tac gcc tgg ttt gat tac aac atg ctg			480
20	Gly Arg Val Cys Ile Ser Leu Tyr Ala Trp Phe Asp Tyr Asn Met Leu			
	145	150	155	
	cac cgc aag cat tgg gag cac cac aac cac act ggc gag gtg ggc aag			528
	His Arg Lys His Trp Glu His His Asn His Thr Gly Glu Val Gly Lys			
25	160	165	170	175
	gac cct gac ttc cac agg gga aac cct ggc att gtg ccc tgg ttt gcc			576
	Asp Pro Asp Phe His Arg Gly Asn Pro Gly Ile Val Pro Trp Phe Ala			
	180	185	190	
30	agc ttc atg tcc agc tac atg tcg atg tgg cag ttt gcg cgc ctc gca			624
	Ser Phe Met Ser Ser Tyr Met Ser Met Trp Gln Phe Ala Arg Leu Ala			
	195	200	205	
35	tgg tgg acg gtg gtc atg cag ctg ctg ggt gcg cca atg gcg aac ctg			672
	Trp Trp Thr Val Val Met Gln Leu Leu Gly Ala Pro Met Ala Asn Leu			
	210	215	220	
	ctg gtg ttc atg gcg gcc gcg ccc atc ctg tcc gcc ttc cgc ttg ttc			720
40	Leu Val Phe Met Ala Ala Ala Pro Ile Leu Ser Ala Phe Arg Leu Phe			
	225	230	235	
	tac ttt ggc acg tac atg ccc cac aag cct gag cct ggc gcc gcg tca			768
	Tyr Phe Gly Thr Tyr Met Pro His Lys Pro Glu Pro Gly Ala Ala Ser			
45	240	245	250	255

ggc tct tca cca gcc gtc atg aac tgg tgg aag tcg cgc act agc cag 816  
 Gly Ser Ser Pro Ala Val Met Asn Trp Trp Lys Ser Arg Thr Ser Gln  
 260 265 270

5

gcg tcc gac ctg gtc agc ttt ctg acc tgc tac cac ttc gac ctg cac 864  
 Ala Ser Asp Leu Val Ser Phe Leu Thr Cys Tyr His Phe Asp Leu His  
 275 280 285

10

tgg gag cac cac cgc tgg ccc ttc gcc ccc tgg tgg gag ctg ccc aac 912  
 Trp Glu His His Arg Trp Pro Phe Ala Pro Trp Trp Glu Leu Pro Asn  
 290 295 300

15

tgc cgc cgc ctg tct ggc cga ggt ctg gtt cct gcc tag ctggacacac 961  
 Cys Arg Arg Leu Ser Gly Arg Gly Leu Val Pro Ala  
 305 310 315

tgcagtgggc cctgctgccg gctgggcatg caggttgtgg caggactggg tgaggtgaaa 1021

20

agctgcaggc gctgctgccg gacacgttgc atgggctacc ctgtgtagct gccgccacta 1081  
 ggggaggggg tttgtagctg tcgagcttgc 1111

25

<210> 25  
 <211> 315  
 <212> PRT

30

<213> Haematococcus pluvialis

35

<400> 25  
 Met Leu Glu Ala Leu Lys Glu Lys Glu Lys Glu Val Ala Gly Ser Ser  
 1 5 10 15

40

Asp Val Leu Arg Thr Trp Ala Thr Gln Tyr Ser Leu Pro Ser Glu Glu  
 20 25 30

45

Ser Asp Ala Ala Arg Pro Gly Leu Lys Asn Ala Tyr Lys Pro Pro Pro

	35	40	45
5	Ser Asp Thr Lys Gly Ile Thr Met Ala Leu Ala Val Ile Gly Ser Trp		
	50	55	60
10	Ala Ala Val Phe Leu His Ala Ile Phe Gln Ile Lys Leu Pro Thr Ser		
	65	70	75 80
15	Leu Asp Gln Leu His Trp Leu Pro Val Ser Asp Ala Thr Ala Gln Leu		
	85	90	95
20	Val Ser Gly Ser Ser Ser Leu Leu His Ile Val Val Val Phe Phe Val		
	100	105	110
25	Leu Glu Phe Leu Tyr Thr Gly Leu Phe Ile Thr Thr His Asp Ala Met		
	115	120	125
30	His Gly Thr Ile Ala Met Arg Asn Arg Gln Leu Asn Asp Phe Leu Gly		
	130	135	140
35	Arg Val Cys Ile Ser Leu Tyr Ala Trp Phe Asp Tyr Asn Met Leu His		
	145	150	155 160
40	Arg Lys His Trp Glu His His Asn His Thr Gly Glu Val Gly Lys Asp		
	165	170	175
45	Pro Asp Phe His Arg Gly Asn Pro Gly Ile Val Pro Trp Phe Ala Ser		
	180	185	190
50	Phe Met Ser Ser Tyr Met Ser Met Trp Gln Phe Ala Arg Leu Ala Trp		
	195	200	205
55	Trp Thr Val Val Met Gln Leu Leu Gly Ala Pro Met Ala Asn Leu Leu		
	210	215	220

Val Phe Met Ala Ala Ala Pro Ile Leu Ser Ala Phe Arg Leu Phe Tyr  
225 230 235 240

5

Phe Gly Thr Tyr Met Pro His Lys Pro Glu Pro Gly Ala Ala Ser Gly  
245 250 255

10

Ser Ser Pro Ala Val Met Asn Trp Trp Lys Ser Arg Thr Ser Gln Ala  
260 265 270

15

Ser Asp Leu Val Ser Phe Leu Thr Cys Tyr His Phe Asp Leu His Trp  
275 280 285

20

Glu His His Arg Trp Pro Phe Ala Pro Trp Trp Glu Leu Pro Asn Cys  
290 295 300

25

Arg Arg Leu Ser Gly Arg Gly Leu Val Pro Ala  
305 310 315

<210> 26

<211> 1031

30

<212> DNA

<213> Haematococcus pluvialis

35

<220>

<221> CDS

40

<222> (6)..(1031)

<223>

<400> 26		
5	gaagc atg cag cta gca gcg aca gta atg ttg gag cag ctt acc gga agc Met Gln Leu Ala Ala Thr Val Met Leu Glu Gln Leu Thr Gly Ser	50
	1 5 10 15	
10	gct gag gca ctc aag gag aag gag aag gag gtt gca ggc agc tct gac Ala Glu Ala Leu Lys Glu Lys Glu Lys Glu Val Ala Gly Ser Ser Asp	98
	20 25 30	
15	gtg ttg cgt aca tgg gcg acc cag tac tcg ctt ccg tca gag gag tca Val Leu Arg Thr Trp Ala Thr Gln Tyr Ser Leu Pro Ser Glu Glu Ser	146
	35 40 45	
20	gac gcg gcc cgc ccg gga ctg aag aat gcc tac aag cca cca cct tcc Asp Ala Ala Arg Pro Gly Leu Lys Asn Ala Tyr Lys Pro Pro Pro Ser	194
	50 55 60	
25	gac aca aag ggc atc aca atg gcg cta gct gtc atc ggc tcc tgg gct Asp Thr Lys Gly Ile Thr Met Ala Leu Ala Val Ile Gly Ser Trp Ala	242
	65 70 75	
30	gca gtg ttc ctc cac gcc att ttt caa atc aag ctt ccg acc tcc ttg Ala Val Phe Leu His Ala Ile Phe Gln Ile Lys Leu Pro Thr Ser Leu	290
	80 85 90 95	
35	gac cag ctg cac tgg ctg ccc gtg tca gat gcc aca gct cag ctg gtt Asp Gln Leu His Trp Leu Pro Val Ser Asp Ala Thr Ala Gln Leu Val	338
	100 105 110	
40	agc ggc agc agc agc ctg ctg cac atc gtc gta gta ttc ttt gtc ctg Ser Gly Ser Ser Ser Ser Leu Leu His Ile Val Val Val Phe Phe Val Leu	386
	115 120 125	
45	gag ttc ctg tac aca ggc ctt ttt atc acc acg cat gat gct atg cat Glu Phe Leu Tyr Thr Gly Leu Phe Ile Thr Thr His Asp Ala Met His	434
	130 135 140	
50	ggc acc atc gcc atg aga aac agg cag ctt aat gac ttc ttg ggc aga Gly Thr Ile Ala Met Arg Asn Arg Gln Leu Asn Asp Phe Leu Gly Arg	482
	145 150 155	
55	gta tgc atc tcc ttg tac gcc tgg ttt gat tac aac atg ctg cac cgc Val Cys Ile Ser Leu Tyr Ala Trp Phe Asp Tyr Asn Met Leu His Arg	530

	160		165		170		175	
	aag cat tgg gag cac cac aac cac act ggc gag gtg ggc aag gac cct							578
	Lys His Trp Glu His His Asn His Thr Gly Glu Val Gly Lys Asp Pro							
5		180		185		190		
	gac ttc cac agg gga aac cct ggc att gtg ccc tgg ttt gcc agc ttc							626
	Asp Phe His Arg Gly Asn Pro Gly Ile Val Pro Trp Phe Ala Ser Phe							
		195		200		205		
10								
	atg tcc agc tac atg tcg atg tgg cag ttt gcg cgc ctc gca tgg tgg							674
	Met Ser Ser Tyr Met Ser Met Trp Gln Phe Ala Arg Leu Ala Trp Trp							
		210		215		220		
15								
	acg gtg gtc atg cag ctg ctg ggt gcg cca atg gcg aac ctg ctg gtg							722
	Thr Val Val Met Gln Leu Leu Gly Ala Pro Met Ala Asn Leu Leu Val							
		225		230		235		
20								
	ttc atg gcg gcc gcg ccc atc ctg tcc gcc ttc cgc ttg ttc tac ttt							770
	Phe Met Ala Ala Ala Pro Ile Leu Ser Ala Phe Arg Leu Phe Tyr Phe							
		240		245		250		255
25								
	ggc acg tac atg ccc cac aag cct gag cct ggc gcc gcg tca ggc tct							818
	Gly Thr Tyr Met Pro His Lys Pro Glu Pro Gly Ala Ala Ser Gly Ser							
		260		265		270		
30								
	tca cca gcc gtc atg aac tgg tgg aag tcg cgc act agc cag gcg tcc							866
	Ser Pro Ala Val Met Asn Trp Trp Lys Ser Arg Thr Ser Gln Ala Ser							
		275		280		285		
35								
	gac ctg gtc agc ttt ctg acc tgc tac cac ttc gac ctg cac tgg gag							914
	Asp Leu Val Ser Phe Leu Thr Cys Tyr His Phe Asp Leu His Trp Glu							
		290		295		300		
40								
	cac cac cgc tgg ccc ttt gcc ccc tgg tgg gag ctg ccc aac tgc cgc							962
	His His Arg Trp Pro Phe Ala Pro Trp Trp Glu Leu Pro Asn Cys Arg							
		305		310		315		
45								
	cgc ctg tct ggc cga ggt ctg gtt cct gcc gag caa aaa ctc atc tca							1010
	Arg Leu Ser Gly Arg Gly Leu Val Pro Ala Glu Gln Lys Leu Ile Ser							
		320		325		330		335
	gaa gag gat ctg aat agc tag							1031
	Glu Glu Asp Leu Asn Ser							
		340						



<210> 27  
 5 <211> 341  
 <212> PRT  
 <213> Haematococcus pluvialis  
 10  
 <400> 27  
 15 Met Gln Leu Ala Ala Thr Val Met Leu Glu Gln Leu Thr Gly Ser Ala  
 1 5 10 15  
 Glu Ala Leu Lys Glu Lys Glu Lys Glu Val Ala Gly Ser Ser Asp Val  
 20 20 25 30  
 Leu Arg Thr Trp Ala Thr Gln Tyr Ser Leu Pro Ser Glu Glu Ser Asp  
 25 35 40 45  
 Ala Ala Arg Pro Gly Leu Lys Asn Ala Tyr Lys Pro Pro Pro Ser Asp  
 50 55 60  
 30 Thr Lys Gly Ile Thr Met Ala Leu Ala Val Ile Gly Ser Trp Ala Ala  
 65 70 75 80  
 35 Val Phe Leu His Ala Ile Phe Gln Ile Lys Leu Pro Thr Ser Leu Asp  
 85 90 95  
 Gln Leu His Trp Leu Pro Val Ser Asp Ala Thr Ala Gln Leu Val Ser  
 40 100 105 110  
 Gly Ser Ser Ser Leu Leu His Ile Val Val Val Phe Phe Val Leu Glu  
 45 115 120 125

Phe Leu Tyr Thr Gly Leu Phe Ile Thr Thr His Asp Ala Met His Gly  
 130 135 140

5  
 Thr Ile Ala Met Arg Asn Arg Gln Leu Asn Asp Phe Leu Gly Arg Val  
 145 150 155 160

10  
 Cys Ile Ser Leu Tyr Ala Trp Phe Asp Tyr Asn Met Leu His Arg Lys  
 165 170 175

15  
 His Trp Glu His His Asn His Thr Gly Glu Val Gly Lys Asp Pro Asp  
 180 185 190

20  
 Phe His Arg Gly Asn Pro Gly Ile Val Pro Trp Phe Ala Ser Phe Met  
 195 200 205

Ser Ser Tyr Met Ser Met Trp Gln Phe Ala Arg Leu Ala Trp Trp Thr  
 210 215 220

25  
 Val Val Met Gln Leu Leu Gly Ala Pro Met Ala Asn Leu Leu Val Phe  
 225 230 235 240

30  
 Met Ala Ala Ala Pro Ile Leu Ser Ala Phe Arg Leu Phe Tyr Phe Gly  
 245 250 255

35  
 Thr Tyr Met Pro His Lys Pro Glu Pro Gly Ala Ala Ser Gly Ser Ser  
 260 265 270

40  
 Pro Ala Val Met Asn Trp Trp Lys Ser Arg Thr Ser Gln Ala Ser Asp  
 275 280 285

Leu Val Ser Phe Leu Thr Cys Tyr His Phe Asp Leu His Trp Glu His  
 290 295 300

45

## 63

His Arg Trp Pro Phe Ala Pro Trp Trp Glu Leu Pro Asn Cys Arg Arg  
 '305 310 315 320

5 Leu Ser Gly Arg Gly Leu Val Pro Ala Glu Gln Lys Leu Ile Ser Glu  
 325 330 335

10 Glu Asp Leu Asn Ser  
 340

<210> 28

15 <211> 777

<212> DNA

20 <213> Arabidopsis thaliana

<220>

25 <221> promoter

<222> (1)..(777)

<223>

30

<400> 28

35 gagctcactc actgatttcc attgcttgaa aattgatgat gaactaagat caatccatgt 60

tagtttcaaa acaacagtaa ctgtggccaa cttagttttg aaacaacact aactgggtcga 120

agcaaaaaga aaaaagagtt tcatcatata tctgatttga tggactggtt ggagtttagga 180

40 ccaaacatta tctacaaaca aagacttttc tcttaacttg tgattccttc ttaaacccta 240

ggggtaatat tctattttcc aaggatcttt agttaaaggc aaatccggga aattattgta 300

45 atcatttggg gaaacatata aaagatttga gttagatgga agtgacgatt aatccaaaca 360

64

tatatatctc tttcttctta tttcccaaat taacagacaa aagtagaata ttggctttta 420  
acaccaatat aaaaacttgc ttcacaccta aacacttttg tttacttttag ggtaagtgca 480  
5 aaaagccaac caaatccacc tgcactgatt tgacgtttac aaacgccgtt aagtcgatgt 540  
ccgttgattt aaacagtgtc ttgtaattaa aaaaatcagt ttacataaat ggaaaattta 600  
tcacttagtt ttcacaaact tctgaactta cttttcatgg attaggcaat actttccatt 660  
10 tttagtaact caagtggacc ctttacttct tcaactccat ctctctcttt ctatttcact 720  
tctttcttct cattatatct cttgtcctct ccaccaaate tcttcaacaa aaagctt 777

15

&lt;210&gt; 29

&lt;211&gt; 22

20

&lt;212&gt; DNA

&lt;213&gt; synthetic

25

&lt;220&gt;

&lt;221&gt; primer\_bind

30

&lt;222&gt; (1)..(22)

&lt;223&gt;

35

&lt;400&gt; 29

gcaagctcga cagctacaaa cc

22

40

&lt;210&gt; 30

&lt;211&gt; 24

&lt;212&gt; DNA

45

<213> synthetic

5 <220>

<221> primer\_bind

<222> (1)..(24)

10

<223>

15

<400> 30  
gaagcatgca gctagcagcg acag

24

20

<210> 31

<211> 30

<212> DNA

25

<213> synthetic

30

<220>

<221> primer\_bind

<222> (1)..(30)

35

<223>

40

<400> 31  
tgcattgctag aggcactcaa ggagaaggag

30

<210> 32

<211> 59

<212> DNA

5 <213> synthetic

<220>

10

<221> primer\_bind

<222> (1)..(59)

15

<223>

<400> 32

20 ctagctattc agatcctctt ctgagatgag tttttgctcg gcaggaacca gacctcggc 59

<210> 33

25

<211> 28

<212> DNA

<213> synthetic

30

<220>

35

<221> primer\_bind

<222> (1)..(28)

<223>

40

<400> 33

45 gagctcactc actgatttcc attgcttg 28

5 <210> 34  
<211> 37  
<212> DNA  
<213> synthetic  
10  
<220>  
<221> primer\_bind  
15 <222> (1)..(37)  
<223>  
20  
<400> 34  
cgccggttaag tcgatgtccg ttgatttaaa cagtgtc 37  
25  
<210> 35  
<211> 34  
30 <212> DNA  
<213> synthetic  
35  
<220>  
<221> primer\_bind  
40 <222> (1)..(34)  
<223>  
45

&lt;400&gt; 35

atcaacggac atcgacttaa cggcgtttgt aaac

34

5 &lt;210&gt; 36

&lt;211&gt; 25

&lt;212&gt; DNA

10

&lt;213&gt; synthetic

15 &lt;220&gt;

&lt;221&gt; primer\_bind

&lt;222&gt; (1)..(25)

20

&lt;223&gt;

25 &lt;400&gt; 36

taagcttttt gttgaagaga tttgg

25

&lt;210&gt; 37

30

&lt;211&gt; 212

&lt;212&gt; DNA

35 &lt;213&gt; Synthetic sequence

&lt;220&gt;

40

&lt;221&gt; Intron

&lt;222&gt; (1)..(212)

45 &lt;223&gt;



<400> 37  
 5 gtcgactacg taagtttctg cttctacctt tgatatatat ataataatta tcattaatta 60  
 gtagtaatat aatatttcaa atattttttt caaaataaaa gaatgtagta tatagcaatt 120  
 gcttttctgt agtttataag tgtgtatatt ttaatttata actttttctaa tatatgacca 180  
 10 aaatttggtg atgtgcaggt atcaccggat cc. 212

<210> 38  
 15 <211> 1830  
 <212> DNA  
 20 <213> Tagetes erecta

<220>  
 25 <221> CDS  
 <222> (141)..(1691)  
 30 <223>

<400> 38  
 35 ggcacgaggc aaagcaaagg ttgtttggtg ttgttggtga gagacactcc aatccaaaca 60  
 gatacaaggc gtgactggat atttctctct cgttcctaac aacagcaacg aagaagaaaa 120  
 agaatcatta ctaacaatca atg agt atg aga gct gga cac atg acg gca aca 173  
 40 Met Ser Met Arg Ala Gly His Met Thr Ala Thr  
 1 5 10  
 atg gcg gct ttt aca tgc cct agg ttt atg act agc atc aga tac acg 221  
 Met Ala Ala Phe Thr Cys Pro Arg Phe Met Thr Ser Ile Arg Tyr Thr  
 45 15 20 25

aag caa att aag tgc aac gct gct aaa agc cag cta gtc gtt aaa caa 269  
 Lys Gln Ile Lys Cys Asn Ala Ala Lys Ser Gln Leu Val Val Lys Gln  
 30 35 40

5

gag att gag gag gaa gaa gat tat gtg aaa gcc ggt gga tgc gag ctg 317  
 Glu Ile Glu Glu Glu Glu Asp Tyr Val Lys Ala Gly Gly Ser Glu Leu  
 45 50 55

10

ctt ttt gtt caa atg caa cag aat aag tcc atg gat gca cag tct agc 365  
 Leu Phe Val Gln Met Gln Gln Asn Lys Ser Met Asp Ala Gln Ser Ser  
 60 65 70 75

15

cta tcc caa aag ctc cca agg gta cca ata gga gga gga gga gac agt 413  
 Leu Ser Gln Lys Leu Pro Arg Val Pro Ile Gly Gly Gly Gly Asp Ser  
 80 85 90

20

aac tgt ata ctg gat ttg gtt gta att ggt tgt ggt cct gct ggc ctt 461  
 Asn Cys Ile Leu Asp Leu Val Val Ile Gly Cys Gly Pro Ala Gly Leu  
 95 100 105

25

gct ctt gct gga gaa tca gcc aag cta ggc ttg aat gtc gca ctt atc 509  
 Ala Leu Ala Gly Glu Ser Ala Lys Leu Gly Leu Asn Val Ala Leu Ile  
 110 115 120

30

ggc cct gat ctt cct ttt aca aat aac tat ggt gtt tgg gag gat gaa 557  
 Gly Pro Asp Leu Pro Phe Thr Asn Asn Tyr Gly Val Trp Glu Asp Glu  
 125 130 135

35

ttt ata ggt ctt gga ctt gag ggc tgt att gaa cat gtt tgg cga gat 605  
 Phe Ile Gly Leu Gly Leu Glu Gly Cys Ile Glu His Val Trp Arg Asp  
 140 145 150 155

40

act gta gta tat ctt gat gac aac gat ccc att ctc ata ggt cgt gcc 653  
 Thr Val Val Tyr Leu Asp Asp Asn Asp Pro Ile Leu Ile Gly Arg Ala  
 160 165 170

45

tat gga cga gtt agt cgt gat tta ctt cac gag gag ttg ttg act agg 701  
 Tyr Gly Arg Val Ser Arg Asp Leu Leu His Glu Glu Leu Leu Thr Arg  
 175 180 185

tgc atg gag tca ggc gtt tca tat ctg agc tcc aaa gtg gaa cgg att 749  
 Cys Met Glu Ser Gly Val Ser Tyr Leu Ser Ser Lys Val Glu Arg Ile  
 190 195 200

71

	act gaa gct cca aat ggc cta agt ctc ata gag tgt gaa ggc aat atc	797
	Thr Glu Ala Pro Asn Gly Leu Ser Leu Ile Glu Cys Glu Gly Asn Ile	
	205 210 215	
5	aca att cca tgc agg ctt gct act gtc gct tct gga gca gct tct gga	845
	Thr Ile Pro Cys Arg Leu Ala Thr Val Ala Ser Gly Ala Ala Ser Gly	
	220 225 230 235	
10	aaa ctt ttg cag tat gaa ctt ggc ggt ccc cgt gtt tgc gtt caa aca	893
	Lys Leu Leu Gln Tyr Glu Leu Gly Gly Pro Arg Val Cys Val Gln Thr	
	240 245 250	
15	gct tat ggt ata gag gtt gag gtt gaa agc ata ccc tat gat cca agc	941
	Ala Tyr Gly Ile Glu Val Glu Val Glu Ser Ile Pro Tyr Asp Pro Ser	
	255 260 265	
20	cta atg gtt ttc atg gat tat aga gac tac acc aaa cat aaa tct caa	989
	Leu Met Val Phe Met Asp Tyr Arg Asp Tyr Thr Lys His Lys Ser Gln	
	270 275 280	
	tca cta gaa gca caa tat cca aca ttt ttg tat gtc atg cca atg tct	1037
	Ser Leu Glu Ala Gln Tyr Pro Thr Phe Leu Tyr Val Met Pro Met Ser	
	285 290 295	
25	cca act aaa gta ttc ttt gag gaa act tgt ttg gct tca aaa gag gcc	1085
	Pro Thr Lys Val Phe Phe Glu Glu Thr Cys Leu Ala Ser Lys Glu Ala	
	300 305 310 315	
30	atg cct ttt gag tta ttg aag aca aaa ctc atg tca aga tta aag act	1133
	Met Pro Phe Glu Leu Leu Lys Thr Lys Leu Met Ser Arg Leu Lys Thr	
	320 325 330	
35	atg ggg atc cga ata acc aaa act tat gaa gag gaa tgg tca tat att	1181
	Met Gly Ile Arg Ile Thr Lys Thr Tyr Glu Glu Glu Trp Ser Tyr Ile	
	335 340 345	
40	cca gta ggt gga tcc tta cca aat acc gag caa aag aac ctt gca ttt	1229
	Pro Val Gly Gly Ser Leu Pro Asn Thr Glu Gln Lys Asn Leu Ala Phe	
	350 355 360	
	ggt gct gct gct agc atg gtg cat cca gcc aca gga tat tcg gtt gta	1277
	Gly Ala Ala Ala Ser Met Val His Pro Ala Thr Gly Tyr Ser Val Val	
	365 370 375	
45	aga tca ctg tca gaa gct cct aat tat gca gca gta att gca aag att	1325

72

Arg Ser Leu Ser Glu Ala Pro Asn Tyr Ala Ala Val Ile Ala Lys Ile  
 380 385 390 395

5 tta ggg aaa gga aat tca aaa cag atg ctt gat cat gga aga tac aca 1373  
 Leu Gly Lys Gly Asn Ser Lys Gln Met Leu Asp His Gly Arg Tyr Thr  
 400 405 410

10 acc aac atc tca aag caa gct tgg gaa aca ctt tgg ccc ctt gaa agg 1421  
 Thr Asn Ile Ser Lys Gln Ala Trp Glu Thr Leu Trp Pro Leu Glu Arg  
 415 420 425

15 aaa aga cag aga gca ttc ttt ctc ttt gga tta gca ctg att gtc cag 1469  
 Lys Arg Gln Arg Ala Phe Phe Leu Phe Gly Leu Ala Leu Ile Val Gln  
 430 435 440

atg gat att gag ggg acc cgc aca ttc ttc cgg act ttc ttc cgc ttg 1517  
 Met Asp Ile Glu Gly Thr Arg Thr Phe Phe Arg Thr Phe Phe Arg Leu  
 445 450 455

20 ccc aca tgg atg tgg tgg ggg ttt ctt gga tct tcg tta tca tca act 1565  
 Pro Thr Trp Met Trp Trp Gly Phe Leu Gly Ser Ser Leu Ser Ser Thr  
 460 465 470 475

25 gac ttg ata ata ttt gcg ttt tac atg ttt atc ata gca ccg cat agc 1613  
 Asp Leu Ile Ile Phe Ala Phe Tyr Met Phe Ile Ile Ala Pro His Ser  
 480 485 490

30 ctg aga atg ggt ctg gtt aga cat ttg ctt tct gac ccg aca gga gga 1661  
 Leu Arg Met Gly Leu Val Arg His Leu Leu Ser Asp Pro Thr Gly Gly  
 495 500 505

35 aca atg tta aaa gcg tat ctc acg ata taa ataactctag tcgcgatcag 1711  
 Thr Met Leu Lys Ala Tyr Leu Thr Ile  
 510 515

tttagattat aggcacatct tgcatatata tatgtataaa ccttatgtgt gctgtatcct 1771

tacatcaaca cagtcattaa ttgtatttct tggggtaatg ctgatgaagt attttctgg 1830

40

&lt;210&gt; 39

&lt;211&gt; 516

&lt;212&gt; PRT

&lt;213&gt; Tagetes erecta

5

&lt;400&gt; 39

Met Ser Met Arg Ala Gly His Met Thr Ala Thr Met Ala Ala Phe Thr  
 10 1 5 10 15

Cys Pro Arg Phe Met Thr Ser Ile Arg Tyr Thr Lys Gln Ile Lys Cys  
 15 20 25 30

Asn Ala Ala Lys Ser Gln Leu Val Val Lys Gln Glu Ile Glu Glu Glu  
 35 40 45

Glu Asp Tyr Val Lys Ala Gly Gly Ser Glu Leu Leu Phe Val Gln Met  
 20 50 55 60

Gln Gln Asn Lys Ser Met Asp Ala Gln Ser Ser Leu Ser Gln Lys Leu  
 25 65 70 75 80

Pro Arg Val Pro Ile Gly Gly Gly Gly Asp Ser Asn Cys Ile Leu Asp  
 30 85 90 95

Leu Val Val Ile Gly Cys Gly Pro Ala Gly Leu Ala Leu Ala Gly Glu  
 35 100 105 110

Ser Ala Lys Leu Gly Leu Asn Val Ala Leu Ile Gly Pro Asp Leu Pro  
 115 120 125

Phe Thr Asn Asn Tyr Gly Val Trp Glu Asp Glu Phe Ile Gly Leu Gly  
 40 130 135 140

Leu Glu Gly Cys Ile Glu His Val Trp Arg Asp Thr Val Val Tyr Leu  
 45

145		150		155		160
5	Asp Asp Asn Asp Pro Ile Leu Ile Gly Arg Ala Tyr Gly Arg Val Ser	165	170	175		
10	Arg Asp Leu Leu His Glu Glu Leu Leu Thr Arg Cys Met Glu Ser Gly	180	185	190		
15	Val Ser Tyr Leu Ser Ser Lys Val Glu Arg Ile Thr Glu Ala Pro Asn	195	200	205		
20	Gly Leu Ser Leu Ile Glu Cys Glu Gly Asn Ile Thr Ile Pro Cys Arg	210	215	220		
25	Leu Ala Thr Val Ala Ser Gly Ala Ala Ser Gly Lys Leu Leu Gln Tyr	225	230	235	240	
30	Glu Leu Gly Gly Pro Arg Val Cys Val Gln Thr Ala Tyr Gly Ile Glu	245	250	255		
35	Val Glu Val Glu Ser Ile Pro Tyr Asp Pro Ser Leu Met Val Phe Met	260	265	270		
40	Asp Tyr Arg Asp Tyr Thr Lys His Lys Ser Gln Ser Leu Glu Ala Gln	275	280	285		
45	Tyr Pro Thr Phe Leu Tyr Val Met Pro Met Ser Pro Thr Lys Val Phe	290	295	300		
	Phe Glu Glu Thr Cys Leu Ala Ser Lys Glu Ala Met Pro Phe Glu Leu	305	310	315	320	
	Leu Lys Thr Lys Leu Met Ser Arg Leu Lys Thr Met Gly Ile Arg Ile	325	330	335		

Thr Lys Thr Tyr Glu Glu Glu Trp Ser Tyr Ile Pro Val Gly Gly Ser  
 340 345 350  
 5

Leu Pro Asn Thr Glu Gln Lys Asn Leu Ala Phe Gly Ala Ala Ala Ser  
 355 360 365

10 Met, Val His Pro Ala Thr Gly Tyr Ser Val Val Arg Ser Leu Ser Glu  
 370 375 380

15 Ala Pro Asn Tyr Ala Ala Val Ile Ala Lys Ile Leu Gly Lys Gly Asn  
 385 390 395 400

20 Ser Lys Gln Met Leu Asp His Gly Arg Tyr Thr Thr Asn Ile Ser Lys  
 405 410 415

25 Gln Ala Trp Glu Thr Leu Trp Pro Leu Glu Arg Lys Arg Gln Arg Ala  
 420 425 430

Phe Phe Leu Phe Gly Leu Ala Leu Ile Val Gln Met Asp Ile Glu Gly  
 435 440 445

30 Thr Arg Thr Phe Phe Arg Thr Phe Phe Arg Leu Pro Thr Trp Met Trp  
 450 455 460

35 Trp Gly Phe Leu Gly Ser Ser Leu Ser Ser Thr Asp Leu Ile Ile Phe  
 465 470 475 480

40 Ala Phe Tyr Met Phe Ile Ile Ala Pro His Ser Leu Arg Met Gly Leu  
 485 490 495

45 Val Arg His Leu Leu Ser Asp Pro Thr Gly Gly Thr Met Leu Lys Ala  
 500 505 510

Tyr Leu Thr Ile

515

5

&lt;210&gt; 40

&lt;211&gt; 445

10

&lt;212&gt; DNA

<213> *Tagetes erecta*

15

&lt;220&gt;

&lt;221&gt; Sense Fragment

20

&lt;222&gt; (1)..(445)

&lt;223&gt;

25

&lt;400&gt; 40

aagcttgac gaggcaaagc aaaggttggt tgttggtggt gttgagagac actccaatcc 60

aaacagatac aaggcgtgac tggatatttc tctctcggtc ctaacaacag caacgaagaa 120

30

gaaaaagaat cactactaac aatcaatgag tatgagagct ggacacatga cggcaacaat 180

ggcggctttt acatgcccta ggtttatgac tagcatcaga tacacgaagc aaattaagtg 240

35

caacgctgct aaaagccagc tagtcgttaa acaagagatt gaggaggaag aagattatgt 300

gaaagccggt ggatcggagc tgctttttgt tcaaatacaa cagaataagt ccatggatgc 360

acagtctagc ctatcccaaa agctccaag ggtaccaata ggaggaggag gagacagtaa 420

40

ctgtatactg gatttggttg tcgac 445

&lt;210&gt; 41

45



&lt;211&gt; 446

&lt;212&gt; DNA

5 &lt;213&gt; Tagetes erecta

&lt;220&gt;

10

&lt;221&gt; Antisense Fragment

&lt;222&gt; (1)..(446)

15

&lt;223&gt;

&lt;400&gt; 41

20

gaattcgac gaggcaaagc aaaggttggt tgttggtggt gttgagagac actccaatcc 60

aaacagatac aaggcgtgac tggatatttc tctctcggtc ctaacaacag caacgaagaa 120

gaaaaagaat cattactaac aatcaatgag tatgagagct ggacacatga cggcaacaat 180

25

ggcggctttt acatgcccta ggtttatgac tagcatcaga tacacgaagc aaattaagtg 240

caacgctgct aaaagccagc tagtcgttaa acaagagatt gaggaggaag aagattatgt 300

30

gaaagccggt ggatcggagc tgctttttgt tcaaagcaa cagaataagt ccatggatgc 360

acagtctagc ctatcccaaa agtcccaag ggtaccaata ggaggaggag gagacagtaa 420

ctgtatactg gatttggttg gacccct 446

35

&lt;210&gt; 42

&lt;211&gt; 393

40

&lt;212&gt; DNA

&lt;213&gt; Tagetes erecta

&lt;220&gt;

5 &lt;221&gt; Sense Fragment

&lt;222&gt; (1)..(393)

&lt;223&gt;

10

&lt;400&gt; 42

15

aagcttttga ttagcactga ttgtccagat ggatattgag gggacccgca cattcttccg 60

gactttcttc cgcttgccca catggatgtg gtggggggtt cttggatctt cgttatcatc 120

aactgacttg ataatatattg cgttttacat gtttatcata gcaccgcata gcctgagaat 180

20 gggctcgggt agacatttgc tttctgaccc gacaggagga acaatgttaa aagcgtatct 240

cacgatataa ataactctag tcgcatcag ttagattat aggcacatct tgcatatata 300

25 tatgtataaa ccttatgtgt gctgtatcct tacatcaaca cagtcattaa ttgtatttct 360

tggggtaatg ctgatgaagt attttctgtc gac 393

&lt;210&gt; 43

30

&lt;211&gt; 397

&lt;212&gt; DNA

35 &lt;213&gt; Tagetes erecta

&lt;220&gt;

40

&lt;221&gt; Antisense Fragment

&lt;222&gt; (1)..(397)

45 &lt;223&gt;

<400> 43  
 5 gaattctctt tggattagca ctgattgtcc agatggatat tgaggggacc cgcacattct 60  
 tccggacttt ctccgcttg cccacatgga tgtggtgggg gtttcttgga tcttcgttat 120  
 catcaactga cttgataata ttgctgtttt acatgtttat catagcaccg catagcctga 180  
 10 gaatgggtct ggtagacat ttgctttctg acccgacagg aggaacaatg ttaaaagcgt 240  
 atctcagat ataaataact ctagtgcga tcagtttaga ttataggcac atcttgcata 300  
 15 tatatatgta taaaccttat gtgtgctgta tccttacatc aacacagtca ttaattgtat 360  
 ttcttggggg aatgctgatg aagtattttc tggatcc 397

20 <210> 44

<211> 1537

25 <212> DNA

<213> -

30 <220>

<221> promoter

<222> (1)..(1537)

35 <223>

40 <400> 44  
 gagctctaca aattaggggt actttattca ttttcatcca ttctctttat tgttaaattt 60  
 tgtacattta ttcaataata ttatatgttt attacaaatt ctcactttct tattcatacc 120  
 45 tattcactca agcctttacc atcttccttt tctatttcaa tactatttct acttcatttt 180

	tcacgttttt aacatctttc ttattttctt gtccacttcg tttagggatg cctaattgtcc	240
	caaatttcat ctctcgtagt aacacaaaaac caatgtaatg ctacttctct ctacattttt	300
5	aatacaaata aagtgaaaca aaatatctat aaataaaca atatatatat tttgttagac	360
	gctgtctcaa cccatcaatt aaaaaatttt gttatatttc tactttacct actaaatttg	420
10	tttctcatat ttacctttta acccccacaa aaaaaaatta taaaaaagaa agaaaaaagc	480
	taaaccttat ttaaatagct aactataaga tcttaaaatt atcctcatca gtgtatagtt	540
	taattggtta ttaacttata acattatata tctatgacat atactctctc ctagctattt	600
15	ctcacatttt ttaacttaag aaaatagtca taacatagtc taaaattcaa acatccacat	660
	gctctaattt gattaacaaa aagttagaaa tattttattha aataaaaaag actaataaat	720
20	atataaaatg aatgttcata cgcagaccca tttagagatg agtatgcttt cacatgctga	780
	gattattttc aaaactaagg ttgtagcaat attaaatcaa taaaattatt ataaataaca	840
	aaattaacct gctcgtgttt gctgtatatg ggaggctaca aaataaatta aactaaagat	900
25	gattatgttt tagacatttt ttctatctgt attagtttat acatattaat tcaggagctg	960
	cacaacccaa ttctattttc gttccttggt ggctgggttt ctcacaaggt tcaatagtca	1020
30	atattagggt ttattggact tttaatagta tcaaacaaat ctatgtgtga acttaaaaat	1080
	tgtattaaat atttagggta acctgttgcc gtttttagaa taatgtttct tcttaataca	1140
	cgaaagcgta ttgtgtattc attcatttgg cgcctcacat gcttcgggtg gctcgtttta	1200
35	gtctctgcct tctttgtata ttgtactccc cctcttccta tgccacgtgt tctgagctta	1260
	acaagccaag ttgcgtgccca ttgccaaaca agtcatttta acttcacaag gtccgatttg	1320
40	acctcaaaa caacgacaag ttccgaaca gtcgcgaaga tcaagggat aatcgtcttt	1380
	ttgaattcta ttctctttta tttaatagtc cctctcgtgt gatagttttt aaaagatttt	1440
45	taaaacgtag ctgctgttta agtaaatccc agtccttcag tttgtgcttt tgtgtgtttt	1500

gtttctctga tttacggaat ttggaaataa taagctt

1537

&lt;210&gt; 45

5

&lt;211&gt; 734

&lt;212&gt; DNA

10 &lt;213&gt; synthetic sequence

&lt;220&gt;

15

&lt;221&gt; variation

&lt;222&gt; (1)..(734)

20 &lt;223&gt;

&lt;400&gt; 45

25

ctaacaatca atgagtagag agctggacac atgacggcaa caatggcggc ttttacatgc 60

cctaggttta tgactagcat cagatacacg aagcaaatta agtgcaacgc tgctaaaagc 120

cagctagtcg ttaaacaaga gattgaggag gaagaagatt atgtgaaagc cggtaggatcg 180

30

gagctgcttt ttgttcaaat gcaacagaat aagtccatgg atgcacagtc tagcctatcc 240

caaaagggtca ctccagactt aattgcttat aaataaataa atatgttttt taggaataat 300

35

gatattttaga tagattagct atcacctgtg ctgtggtgtg cagctcccaa gggctcttacc 360

gatagtaaaa tcgttagtta tgattaatac ttgggaggtg ggggattata ggctttgttg 420

tgagaatggt gagaaagagg ttgacaaat cgggtgttga atgagggttaa atggagttaa 480

40

attaaaataa agagaagaga aagattaaga ggggtgatggg gatattaaag acggscaata 540

tagtgatgcc acgtagaaaa aggtaagtga aaacatacaa cgtggcttta aaagatggct 600

45

tggctgctaa tcaactcaac tcaactcata tcctatccat tcaaattcaa ttcaattcta 660

ttgaatgcaa agcaaagcaa aggttgtttg ttgttgttgt tgagagacac tccaatccaa 720  
 acagatacaa ggcg 734  
 5  
 <210> 46  
 <211> 280  
 10  
 <212> DNA  
 <213> synthetic sequence  
 15  
 <220>  
 <221> variation  
 20  
 <222> (1)..(280)  
 <223>  
 25  
 <400> 46  
 gtcgagtatg gagttcaatt aaaataaaga gaagaaaaag attaagaggg tgatggggat 60  
 30 attaaagacg gccaatrtag tgatgccacg taagaaaaag gtaagtgaac acatacaacg 120  
 tggctttaa agatggcttg gctgctaata aactcaactc aactcatatc ctatccattc 180  
 aaattcaatt caattctatt gaatgcaaag caaagcaaag caaagggttg ttgttgttgt 240  
 35 tgttgagaga cactccaata caaacagata caaggcgtga 280  
 <210> 47  
 40  
 <211> 358  
 <212> DNA

<213> Tagetes erecta

5 <220>

<221> Sense Promoter

<222> (1) .. (358)

10

<223>

15

<400> 47

aagcttaccg atagtaaaat cgtaggttat gattaatact tgggaggtgg gggattatag 60

gctttgttgt gagaatgttg agaaagaggt ttgacaaatc ggtgtttgaa tgagggttaa 120

20

tggagtttaa ttaaaataaa gagaagagaa agattaagag ggtgatgggg atattaaaga 180

cggccaatat agtgatgcca cgtagaaaaa ggtaagtga aacatacaac gtggctttaa 240

aagatggctt ggctgctaact caactcaact caactcatat cctatccatt caaattcaat 300

25

tcaattctat tgaatgcaaa gcaaagcaaa gcaaaggttg tttgttggtg ttgtcgac 358

<210> 48

30

<211> 361

<212> DNA

35

<213> Tagetes erecta

<220>

40

<221> Antisense Promoter

<222> (1) .. (361)

45

<223>

<400> 48  
 5 ctcgagctta ccgatatga aatcgtagt tatgattaat acttgggagg tgggggatta 60  
 taggctttgt tgtgagaatg ttgagaaaga ggtttgacaa atcgggtgtt gaatgagggt 120  
 aaatggaggt taattaaaat aaagagaaga gaaagattaa gagggatgat gggatattaa 180  
 10 agacggccaa tatagtgatg ccacgtagaa aaaggtaagt gaaaacatac aacgtggctt 240  
 taaaagatgg cttggctgct aatcaactca actcaactca taccctatcc attcaaattc 300  
 15 aattcaattc tattgaatgc aaagcaaagc aaagcaaagg ttgtttgttg ttgttgatc 360  
 c 361

20 <210> 49

<211> 28

<212> DNA

25

<213> synthetic sequence

30 <220>

<221> Primer

<222> (1)..(28)

35

<223>

40 <400> 49

gagctcactc actgatttcc attgcttg

28

<210> 50

45



<211> 37

<212> DNA

5 <213> synthetic sequence

<220>

10

<221> Primer

<222> (1)..(37)

15

<223>

<400> 50

20 cgccggttaag tcgatgtccg ttgatttaaa cagtgtc

37

<210> 51

25

<211> 34

<212> DNA

<213> synthetic sequence

30

<220>

35

<221> Primer

<222> (1)..(34)

<223>

40

<400> 51

45 atcaacggac atcgacttaa cggcgtttgt aaac

34

5  
10  
15  
20  
25  
30  
35  
40  
45

<210> 52  
<211> 25  
<212> DNA  
<213> synthetic sequence  
<220>  
<221> Primer  
<222> (1)..(25)  
<223>  
<400> 52  
taagcttttt gttgaagaga tttgg  
<210> 53  
<211> 23  
<212> DNA  
<213> synthetic sequence  
<220>  
<221> Primer  
<222> (1)..(23)  
<223>

25

&lt;400&gt; 53

gaaaatacctt catcagcatt acc

23

5 &lt;210&gt; 54

&lt;211&gt; 28

&lt;212&gt; DNA

10

&lt;213&gt; synthetic sequence

15 &lt;220&gt;

&lt;221&gt; Primer

&lt;222&gt; (1)..(28)

20

&lt;223&gt;

25 &lt;400&gt; 54

gtcgactacg taagtttctg cttctacc

28

&lt;210&gt; 55

30

&lt;211&gt; 26

&lt;212&gt; DNA

35 &lt;213&gt; synthetic sequence

&lt;220&gt;

40

&lt;221&gt; Primer

&lt;222&gt; (1)..(26)

45 &lt;223&gt;

5 <400> 55  
ggatccggtg atacctgcac atcaac

26

<210> 56

10 <211> 28

<212> DNA

15 <213> synthetic sequence

<220>

20 <221> Primer

<222> (1) .. (28)

<223>

25

30 <400> 56  
aagcttgac gaggcaaagc aaaggttg

28

<210> 57

<211> 29

35

<212> DNA

<213> synthetic sequence

40

<220>

<221> Primer

45

<222> (1)..(29)

<223>

5

<400> 57

gtcgacaacc aaatccagta tacagttac

29

10

<210> 58

<211> 30

15

<212> DNA

<213> synthetic sequence

20

<220>

<221> Primer

25

<222> (1)..(30)

<223>

30

<400> 58

aggatccaac caaatccagt atacagttac

30

35

<210> 59

<211> 28

<212> DNA

40

<213> synthetic sequence

<220>

<221> Primer

5 <222> (1)..(28)

<223>

10

<400> 59

gaattcgcac gaggcaaagc aaagggttg

28

15

<210> 60

<211> 25

<212> DNA

20

<213> synthetic sequence

25

<220>

<221> Primer

<222> (1)..(25)

30

<223>

35

<400> 60

aagctttgga ttagcactga ttgtc

25

40

<210> 61

<211> 29

<212> DNA

<213> synthetic sequence

5 <220>

<221> Primer

<222> (1)..(29)

10

<223>

15

<400> 61

gtcgacagaa aatacttcat cagcattac

29

20

<210> 62

<211> 29

<212> DNA

25

<213> synthetic sequence

30

<220>

<221> Primer

<222> (1)..(29)

35

<223>

40

<400> 62

ggatccagaa aatacttcat cagcattac

29

<210> 63

<211> 27

<212> DNA

5 <213> synthetic sequence

<220>

10

<221> Primer

<222> (1)..(27)

15

<223>

<400> 63

20 gaattctctt tggattagca ctgattg

27

<210> 64

25

<211> 23

<212> DNA

<213> synthetic sequence

30

<220>

35

<221> Primer

<222> (1)..(23)

<223>

40

<400> 64

45 cgccttgat ctgtttggat tgg

23



<210> 65

<211> 24

5

<212> DNA

<213> synthetic sequence

10

<220>

<221> Primer

15

<222> (1)..(24)

<223>

20

<400> 65

ctaacaatca atgagtatga gagc

24

25

<210> 66

<211> 26

30

<212> DNA

<213> synthetic sequence

35

<220>

<221> Primer

40

<222> (1)..(26)

<223>

45

<400> 66  
agagcaaggc cagcaggacc acaacc

26

5 <210> 67

<211> 26

<212> DNA

10

<213> synthetic sequence

15 <220>

<221> Primer

<222> (1)..(26)

20

<223>

25 <400> 67

ccttgggagc ttttgggata ggctag

26

<210> 68

30

<211> 26

<212> DNA

35 <213> synthetic sequence

<220>

40

<221> Primer

<222> (1)..(26)

45 <223>

&lt;400&gt; 68

5 tcacgccttg tatctgtttg gattgg

26

&lt;210&gt; 69

10 &lt;211&gt; 15

&lt;212&gt; DNA

&lt;213&gt; , synthetic sequence

15

&lt;220&gt;

20 &lt;221&gt; Primer

&lt;222&gt; (1)..(15)

&lt;223&gt;

25

&lt;400&gt; 69

30 gtcgagtatg gagtt

15

&lt;210&gt; 70

&lt;211&gt; 28

35

&lt;212&gt; DNA

&lt;213&gt; synthetic sequence

40

&lt;220&gt;

&lt;221&gt; Primer

45

<222> (1)..(28)

<223>

5

<400> 70

aagcttaccg atagtaaaat cgttagtt

28

10

<210> 71

<211> 31

15

<212> DNA

<213> synthetic sequence

20

<220>

<221> Primer

25

<222> (1)..(31)

<223>

30

<400> 71

ctcgagctta ccgatagtaa aatcgtagt t

31

35

<210> 72

<211> 28

<212> DNA

40

<213> synthetic sequence

45

<400> 72

gtcgacaaca acaacaaaca acctttgc

28

&lt;210&gt; 73

5

&lt;211&gt; 28

&lt;212&gt; DNA

10 &lt;213&gt; synthetic sequence

&lt;220&gt;

15

&lt;221&gt; Primer

&lt;222&gt; (1)..(28)

20

&lt;223&gt;

&lt;400&gt; 73

25

ggatccaaca acaacaaaca acctttgc

28

&lt;210&gt; 74

30

&lt;211&gt; 28

&lt;212&gt; DNA

&lt;213&gt; synthetic sequence

35

&lt;220&gt;

40

&lt;221&gt; Primer

&lt;222&gt; (1)..(28)

&lt;223&gt;

45

5 <400> 74  
gtcgcactttt tgttgaagag atttggtg

28

10 <210> 75

<211> 28

<212> DNA

<213> synthetic sequence

15

<220>

<221> Primer

20

<222> (1)..(28)..

<223>

25

<400> 75

ctcgagactc actgatttcc attgcttg

28

30

<210> 76

<211> 22

35 <212> DNA

<213> synthetic sequence

40

<220>

<221> Primer

<222> (1)..(22)

<223>

5

<400> 76

gagctctaca aattagggtt ac

22

10

<210> 77

<211> 23

15

<212> DNA

<213> synthetic sequence

20

<220>

<221> Primer

25

<222> (1)..(23)

<223>

30

<400> 77

aagcttatta tttccaaatt ccg

23

35

<210> 78

<211> 50

<212> DNA

40

<213> synthetic sequence

&lt;220&gt;

&lt;221&gt; Primer

5 &lt;222&gt; (1)..(50)

&lt;223&gt;

10

&lt;400&gt; 78

aagctttgca attcatacag aagtgagaaa aatgcagcta gcagcgacag

50

15

&lt;210&gt; 79

&lt;211&gt; 1062

&lt;212&gt; DNA

20

&lt;213&gt; Haematococcus pluvialis

25

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (32)..(1021)

30

&lt;223&gt;

35

&lt;400&gt; 79

aagctttgca attcatacag aagtgagaaa a atg cag cta gca gcg aca gta

52

Met Gln Leu Ala Ala Thr Val

1

5

40

atg ttg gag cag ctt acc gga agc gct gag gca ctc aag gag aag gag

100

Met Leu Glu Gln Leu Thr Gly Ser Ala Glu Ala Leu Lys Glu Lys Glu

10

15

20

aag gag gtt gca ggc agc tct gac gtg ttg cgt aca tgg gcg acc cag

148

45

Lys Glu Val Ala Gly Ser Ser Asp Val Leu Arg Thr Trp Ala Thr Gln



	25	30	35	
	tac tcg ctt ccg tca gag gag tca gac gcg gcc cgc ccg gga ctg aag			196
5	Tyr Ser Leu Pro Ser Glu Glu Ser Asp Ala Ala Arg Pro Gly Leu Lys			
	40	45	50	55
	aat gcc tac aag cca cca cct tcc gac aca aag ggc atc aca atg gcg			244
	Asn Ala Tyr Lys Pro Pro Pro Ser Asp Thr Lys Gly Ile Thr Met Ala			
10		60	65	70
	cta gct gtc atc ggc tcc tgg gcc gca gtg ttc ctc cac gcc att ttt			292
	Leu Ala Val Ile Gly Ser Trp Ala Ala Val Phe Leu His Ala Ile Phe			
	75	80	85	
15	caa atc aag ctt ccg acc tcc ttg gac cag ctg cac tgg ctg ccc gtg			340
	Gln Ile Lys Leu Pro Thr Ser Leu Asp Gln Leu His Trp Leu Pro Val			
	90	95	100	
	tca gat gcc aca gct cag ctg gtt agc ggc agc agc agc ctg ctg cac			388
20	Ser Asp Ala Thr Ala Gln Leu Val Ser Gly Ser Ser Ser Leu Leu His			
	105	110	115	
	atc gtc gta gta ttc ttt gtc ctg gag ttc ctg tac aca ggc ctt ttt			436
	Ile Val Val Val Phe Phe Val Leu Glu Phe Leu Tyr Thr Gly Leu Phe			
25	120	125	130	135
	atc acc acg cat gat gct atg cat ggc acc atc gcc atg aga aac agg			484
	Ile Thr Thr His Asp Ala Met His Gly Thr Ile Ala Met Arg Asn Arg			
	140	145	150	
30	cag ctt aat gac ttc ttg ggc aga gta tgc atc tcc ttg tac gcc tgg			532
	Gln Leu Asn Asp Phe Leu Gly Arg Val Cys Ile Ser Leu Tyr Ala Trp			
	155	160	165	
35	ttt gat tac aac atg ctg cac cgc aag cat tgg gag cac cac aac cac			580
	Phe Asp Tyr Asn Met Leu His Arg Lys His Trp Glu His His Asn His			
	170	175	180	
	act ggc gag gtg ggc aag gac cct gac ttc cac agg gga aac cct ggc			628
40	Thr Gly Glu Val Gly Lys Asp Pro Asp Phe His Arg Gly Asn Pro Gly			
	185	190	195	
	att gtg ccc tgg ttt gcc agc ttc atg tcc agc tac atg tcg atg tgg			676
	Ile Val Pro Trp Phe Ala Ser Phe Met Ser Ser Tyr Met Ser Met Trp			
45	200	205	210	215

cag ttt gcg cgc ctc gca tgg tgg acg gtg gtc atg cag ctg ctg ggt 724  
 Gln Phe Ala Arg Leu Ala Trp Trp Thr Val Val Met Gln Leu Leu Gly  
 220 225 230

5

gcg cca atg gcg aac ctg ctg gtg ttc atg gcg gcc gcg ccc atc ctg 772  
 Ala Pro Met Ala Asn Leu Leu Val Phe Met Ala Ala Ala Pro Ile Leu  
 235 240 245

10

tcc gcc ttc cgc ttg ttc tac ttt ggc acg tac atg ccc cac aag cct 820  
 Ser Ala Phe Arg Leu Phe Tyr Phe Gly Thr Tyr Met Pro His Lys Pro  
 250 255 260

15

gag cct ggc gcc gcg tca ggc tct tca cca gcc gtc atg aac tgg tgg 868  
 Glu Pro Gly Ala Ala Ser Gly Ser Ser Pro Ala Val Met Asn Trp Trp  
 265 270 275

20

aag tcg cgc act agc cag gcg tcc gac ctg gtc agc ttt ctg acc tgc 916  
 Lys Ser Arg Thr Ser Gln Ala Ser Asp Leu Val Ser Phe Leu Thr Cys  
 280 285 290 295

25

tac cac ttc gac ctg cac tgg gag cac cac cgc tgg ccc ttt gcc ccc 964  
 Tyr His Phe Asp Leu His Trp Glu His His Arg Trp Pro Phe Ala Pro  
 300 305 310

30

tgg tgg gag ctg ccc aac tgc cgc cgc ctg tct ggc cga ggt ctg gtt 1012  
 Trp Trp Glu Leu Pro Asn Cys Arg Arg Leu Ser Gly Arg Gly Leu Val  
 315 320 325

35

cct gcc tag ctggacacac tgcagtgggc cctgctgccca gctgggcatg c 1062  
 Pro Ala

40

<210> 80  
 <211> 329  
 <212> PRT  
 <213> Haematococcus pluvialis

45

<400> 80

Met Gln Leu Ala Ala Thr Val Met Leu Glu Gln Leu Thr Gly Ser Ala  
 1 5 10 15  
 5  
 Glu Ala Leu Lys Glu Lys Glu Lys Glu Val Ala Gly Ser Ser Asp Val  
 20 25 30  
 10 Leu Arg Thr Trp Ala Thr Gln Tyr Ser Leu Pro Ser Glu Glu Ser Asp  
 35 40 45  
 15 Ala Ala Arg Pro Gly Leu Lys Asn Ala Tyr Lys Pro Pro Pro Ser Asp  
 50 55 60  
 20 Thr Lys Gly Ile Thr Met Ala Leu Ala Val Ile Gly Ser Trp Ala Ala  
 65 70 75 80  
 Val Phe Leu His Ala Ile Phe Gln Ile Lys Leu Pro Thr Ser Leu Asp  
 85 90 95  
 25 Gln Leu His Trp Leu Pro Val Ser Asp Ala Thr Ala Gln Leu Val Ser  
 100 105 110  
 30 Gly Ser Ser Ser Leu Leu His Ile Val Val Val Phe Phe Val Leu Glu  
 115 120 125  
 35 Phe Leu Tyr Thr Gly Leu Phe Ile Thr Thr His Asp Ala Met His Gly  
 130 135 140  
 40 Thr Ile Ala Met Arg Asn Arg Gln Leu Asn Asp Phe Leu Gly Arg Val  
 145 150 155 160  
 Cys Ile Ser Leu Tyr Ala Trp Phe Asp Tyr Asn Met Leu His Arg Lys  
 165 170 175  
 45

104

His Trp Glu His His Asn His Thr Gly Glu Val Gly Lys Asp Pro Asp  
 180 185 190

5 Phe His Arg Gly Asn Pro Gly Ile Val Pro Trp Phe Ala Ser Phe Met  
 195 200 205

10 Ser Ser Tyr Met Ser Met Trp Gln Phe Ala Arg Leu Ala Trp Trp Thr  
 210 215 220

15 Val Val Met Gln Leu Leu Gly Ala Pro Met Ala Asn Leu Leu Val Phe  
 225 230 235 240

20 Met Ala Ala Ala Pro Ile Leu Ser Ala Phe Arg Leu Phe Tyr Phe Gly  
 245 250 255

Thr Tyr Met Pro His Lys Pro Glu Pro Gly Ala Ala Ser Gly Ser Ser  
 260 265 270

25 Pro Ala Val Met Asn Trp Trp Lys Ser Arg Thr Ser Gln Ala Ser Asp  
 275 280 285

30 Leu Val Ser Phe Leu Thr Cys Tyr His Phe Asp Leu His Trp Glu His  
 290 295 300

35 His Arg Trp Pro Phe Ala Pro Trp Trp Glu Leu Pro Asn Cys Arg Arg  
 305 310 315 320

40 Leu Ser Gly Arg Gly Leu Val Pro Ala  
 325

<210> 81

<211> 789

&lt;212&gt; DNA

&lt;213&gt; Nostoc punctiforme

5

&lt;220&gt;

&lt;221&gt; CDS

10

&lt;222&gt; (1)..(789)

&lt;223&gt;

15

&lt;400&gt; 81

ttg aat ttt tgt gat aaa cca gtt agc tat tat gtt gca ata gag caa 48

Leu Asn Phe Cys Asp Lys Pro Val Ser Tyr Tyr Val Ala Ile Glu Gln

20

1 5 10 15

tta agt gct aaa gaa gat act gtt tgg ggg ctg gtg' att gtc ata gta 96

Leu Ser Ala Lys Glu Asp Thr Val Trp Gly Leu Val Ile Val Ile Val

20 25 30

25

att att agt ctt tgg gta gct agt ttg gct ttt tta cta gct att aat 144

Ile Ile Ser Leu Trp Val Ala Ser Leu Ala Phe Leu Leu Ala Ile Asn

35 40 45

30

tat gcc aaa gtc cca att tgg ttg ata cct att gca ata gtt tgg caa 192

Tyr Ala Lys Val Pro Ile Trp Leu Ile Pro Ile Ala Ile Val Trp Gln

50 55 60

35

atg ttc ctt tat aca ggg cta ttt att act gca cat gat gct atg cat 240

Met Phe Leu Tyr Thr Gly Leu Phe Ile Thr Ala His Asp Ala Met His

65 70 75 80

40

ggg tca gtt tat cgt aaa aat ccc aaa att aat aat ttt atc ggt tca 288

Gly Ser Val Tyr Arg Lys Asn Pro Lys Ile Asn Asn Phe Ile Gly Ser

85 90 95

cta gct gta gcg ctt tac gct gtg ttt cca tat caa cag atg tta aag 336

Leu Ala Val Ala Leu Tyr Ala Val Phe Pro Tyr Gln Gln Met Leu Lys

100 105 110

45

## 106

aat cat tgc tta cat cat cgt cat cct gct agc gaa gtt gac cca gat 384  
 Asn His Cys Leu His His Arg His Pro Ala Ser Glu Val Asp Pro Asp  
 115 120 125

5 ttt cat gat ggt aag aga aca aac gct att ttc tgg tat ctc cat ttc 432  
 Phe His Asp Gly Lys Arg Thr Asn Ala Ile Phe Trp Tyr Leu His Phe  
 130 135 140

10 atg ata gaa tac tcc agt tgg caa cag tta ata gta cta act atc cta 480  
 Met Ile Glu Tyr Ser Ser Trp Gln Gln Leu Ile Val Leu Thr Ile Leu  
 145 150 155 160

15 ttt aat tta gct aaa tac gtt ttg cac atc cat caa ata aat ctc atc 528  
 Phe Asn Leu Ala Lys Tyr Val Leu His Ile His Gln Ile Asn Leu Ile  
 165 170 175

20 tta ttt tgg agt att cct cca att tta agt tcc att caa ctg ttt tat 576  
 Leu Phe Trp Ser Ile Pro Pro Ile Leu Ser Ser Ile Gln Leu Phe Tyr  
 180 185 190

ttc gga aca ttt ttg cct cat cga gaa ccc aag aaa gga tat gtt tat 624  
 Phe Gly Thr Phe Leu Pro His Arg Glu Pro Lys Lys Gly Tyr Val Tyr  
 195 200 205

25 ccc cat tgc agc caa aca ata aaa ttg cca act ttt ttg tca ttt atc 672  
 Pro His Cys Ser Gln Thr Ile Lys Leu Pro Thr Phe Leu Ser Phe Ile  
 210 215 220

30 gct tgc tac cac ttt ggt tat cat gaa gaa cat cat gag tat ccc cat 720  
 Ala Cys Tyr His Phe Gly Tyr His Glu Glu His His Glu Tyr Pro His  
 225 230 235 240

35 gta cct tgg tgg caa ctt cca tct gta tat aag cag aga gta ttc aac 768  
 Val Pro Trp Trp Gln Leu Pro Ser Val Tyr Lys Gln Arg Val Phe Asn  
 245 250 255

40 aat tca gta acc aat tcg taa 789  
 Asn Ser Val Thr Asn Ser  
 260

&lt;210&gt; 82

&lt;211&gt; 262

45

&lt;212&gt; PRT

&lt;213&gt; Nostoc punctiforme

5

&lt;400&gt; 82

10 Leu Asn Phe Cys Asp Lys Pro Val Ser Tyr Tyr Val Ala Ile Glu Gln  
1 5 10 15

15 Leu Ser Ala Lys Glu Asp Thr Val Trp Gly Leu Val Ile Val Ile Val  
20 25 30

Ile Ile Ser Leu Trp Val Ala Ser Leu Ala Phe Leu Leu Ala Ile Asn  
35 40 45

20 Tyr Ala Lys Val Pro Ile Trp Leu Ile Pro Ile Ala Ile Val Trp Gln  
50 55 60

25 Met Phe Leu Tyr Thr Gly Leu Phe Ile Thr Ala His Asp Ala Met His  
65 70 75 80

30 Gly Ser Val Tyr Arg Lys Asn Pro Lys Ile Asn Asn Phe Ile Gly Ser  
85 90 95

35 Leu Ala Val Ala Leu Tyr Ala Val Phe Pro Tyr Gln Gln Met Leu Lys  
100 105 110

Asn His Cys Leu His His Arg His Pro Ala Ser Glu Val Asp Pro Asp  
115 120 125

40 Phe His Asp Gly Lys Arg Thr Asn Ala Ile Phe Trp Tyr Leu His Phe  
130 135 140

45 Met Ile Glu Tyr Ser Ser Trp Gln Gln Leu Ile Val Leu Thr Ile Leu

## 108

145                      150                      155                      160

Phe Asn Leu Ala Lys Tyr Val Leu His Ile His Gln Ile Asn Leu Ile  
5                      165                      170                      175

Leu Phe Trp Ser Ile Pro Pro Ile Leu Ser Ser Ile Gln Leu Phe Tyr  
10                      180                      185                      190

Phe Gly Thr Phe Leu Pro His Arg Glu Pro Lys Lys Gly Tyr Val Tyr  
15                      195                      200                      205

Pro His Cys Ser Gln Thr Ile Lys Leu Pro Thr Phe Leu Ser Phe Ile  
20                      210                      215                      220

Ala Cys Tyr His Phe Gly Tyr His Glu Glu His His Glu Tyr Pro His  
25                      225                      230                      235                      240

Val Pro Trp Trp Gln Leu Pro Ser Val Tyr Lys Gln Arg Val Phe Asn  
30                      245                      250                      255

Asn Ser Val Thr Asn Ser  
35                      260

<210> 83

<211> 762

<212> DNA

<213> Nostoc punctiforme

<220>

<221> CDS

45



$\langle 223 \rangle$

<400> 83

Val Ile Gln Leu Glu Gln Pro Leu Ser His Gln Ala Lys Leu Thr Pro

1

5

10

15

Val Leu Arg Ser Lys Ser Gln Phe Lys Gly Leu Phe Ile Ala Ile Val

20

25

30

att gtt agc gca tgg gtc att agc ctg agt tta tta ctt tcc ctt gac 144

Ile Val Ser Ala Trp Val Ile Ser Leu Ser Leu Leu Leu Ser Leu Asp

35

40

45

atc tca aag cta aaa ttt tgg atg tta ttg cct gtt ata cta tgg caa. 192

Ile Ser Lys Leu Lys' Phe Trp Met Leu. Leu Pro Val Ile Leu Trp Gln

50

55

60

Thr Phe Leu Tyr Thr Gly Leu Phe Ile Thr Ser His Asp Ala Met His

65

70

75

80

Gly Val Val Phe Pro Gln Asn Thr Lys Ile Asn His Leu Ile Gly Thr

85

90

95

Leu Thr Leu Ser Leu Tyr Gly Leu Leu Pro Tyr Gln Lys Leu Leu Lys

100

105

110

aaa cat tgg tta cac cac cac aat cca gca agc tca ata gac ccg gat 384

Lys His Trp Leu His His His Asn Pro Ala Ser Ser Ile Asp Pro Asp

115

120

125

ttt cac aat ggt aaa cac caa agt ttc ttt gct tgg tat ttt cat ttt 432

Phe His Asn Gly Lys His Gln Ser Phe Phe Ala Trp Tyr Phe His Phe

130

135

140

Met Lys Gly Tyr Trp Ser Trp Gly Gln Ile Ile Ala Leu Thr Ile Ile

45

110

	145	150	155	160	
	tat aac ttt gct aaa tac ata ctc cat atc cca agt gat aat cta act				528
	Tyr Asn Phe Ala Lys Tyr Ile Leu His Ile Pro Ser Asp Asn Leu Thr				
5		165	170	175	
	tac ttt tgg gtg cta ccc tcg ctt tta agt tca tta caa tta ttc tat				576
	Tyr Phe Trp Val Leu Pro Ser Leu Leu Ser Ser Leu Gln Leu Phe Tyr				
	180		185	190	
10	ttt ggt act ttt tta ccc cat agt gaa cca ata ggg ggt tat gtt cag				624
	Phe Gly Thr Phe Leu Pro His Ser Glu Pro Ile Gly Gly Tyr Val Gln				
	195		200	205	
15	cct cat tgt gcc caa aca att agc cgt cct att tgg tgg tca ttt atc				672
	Pro His Cys Ala Gln Thr Ile Ser Arg Pro Ile Trp Trp Ser Phe Ile				
	210		215	220	
	acg tgc tat cat ttt ggc tac cac gag gaa cat cac gaa tat cct cat				720
20	Thr Cys Tyr His Phe Gly Tyr His Glu Glu His His Glu Tyr Pro His				
	225		230	235	240
	att tct tgg tgg cag tta cca gaa att tac aaa gca aaa tag				762
	Ile Ser Trp Trp Gln Leu Pro Glu Ile Tyr Lys Ala Lys				
25		245	250		
	<210> 84				
30	<211> 253				
	<212> PRT				
	<213> Nostoc punctiforme				
35					
	<400> 84				
40	Val Ile Gln Leu Glu Gln Pro Leu Ser His Gln Ala Lys Leu Thr Pro				
	1	5	10	15	
	Val Leu Arg Ser Lys Ser Gln Phe Lys Gly Leu Phe Ile Ala Ile Val				
45	20		25	30	

Ile Val Ser Ala Trp Val Ile Ser Leu Ser Leu Leu Leu Ser Leu Asp  
 35 40 45  
 5

Ile Ser Lys Leu Lys Phe Trp Met Leu Leu Pro Val Ile Leu Trp Gln  
 50 55 60

10

Thr Phe Leu Tyr Thr Gly Leu Phe Ile Thr Ser His Asp Ala Met His  
 65 70 75 80

15

Gly Val Val Phe Pro Gln Asn Thr Lys Ile Asn His Leu Ile Gly Thr  
 85 90 95

20

Leu Thr Leu Ser Leu Tyr Gly Leu Leu Pro Tyr Gln Lys Leu Leu Lys  
 100 105 110

25

Lys His Trp Leu His His His Asn Pro Ala Ser Ser Ile Asp Pro Asp  
 115 120 125

30

Phe His Asn Gly Lys His Gln Ser Phe Phe Ala Trp Tyr Phe His Phe  
 130 135 140

35

Met Lys Gly Tyr Trp Ser Trp Gly Gln Ile Ile Ala Leu Thr Ile Ile  
 145 150 155 160

40

Tyr Asn Phe Ala Lys Tyr Ile Leu His Ile Pro Ser Asp Asn Leu Thr  
 165 170 175

45

Tyr Phe Trp Val Leu Pro Ser Leu Leu Ser Ser Leu Gln Leu Phe Tyr  
 180 185 190

Phe Gly Thr Phe Leu Pro His Ser Glu Pro Ile Gly Gly Tyr Val Gln  
 195 200 205

Pro His Cys Ala Gln Thr Ile Ser Arg Pro Ile Trp Trp Ser Phe Ile  
 210 215 220

5

Thr Cys Tyr His Phe Gly Tyr His Glu Glu His His Glu Tyr Pro His  
 225 230 235 240

10

Ile Ser Trp Trp Gln Leu Pro Glu Ile Tyr Lys Ala Lys  
 245 250

<210> .85

15

<211> 804

<212> DNA

20

<213> Synechococcus WH8102

<220>

25

<221> CDS

<222> (1)..(804)

30

<223>

<400> 85

35

atg aaa acg aca aga tct att tcg tgg cca tcg act tgc tgg cat cac 48  
 Met Lys Thr Thr Arg Ser Ile Ser Trp Pro Ser Thr Cys Trp His His  
 1 5 10 15

cag ccg agt tgc tca agc tgg gtg gca aat gag ttc agc cct cag gcc 96

40

Gln Pro Ser Cys Ser Ser Trp Val Ala Asn Glu Phe Ser Pro Gln Ala  
 20 25 30

ctc aaa ggg ttg gct ctg gct ggt ctg att gga tca gcc tgg ctg ctc 144  
 Leu Lys Gly Leu Ala Leu Ala Gly Leu Ile Gly Ser Ala Trp Leu Leu  
 45 35 40 45

113

	tcc ctg ggc ctg agc tac acc ctg cca ctt gat cag acg cct ggg ctg	192
	Ser Leu Gly Leu Ser Tyr Thr Leu Pro Leu Asp Gln Thr Pro Gly Leu	
	50 55 60	
5	ttg att ggc agc ttg att ctg ctc aga gca ttt ctg cac acc ggg ctg	240
	Leu Ile Gly Ser Leu Ile Leu Leu Arg Ala Phe Leu His Thr Gly Leu	
	65 70 75 80	
10	ttc atc gtt gcc cac gat tcc atg cac gcc agt ctg gtt ccg ggt cat	288
	Phe Ile Val Ala His Asp Ser Met His Ala Ser Leu Val Pro Gly His	
	85 90 95	
15	ccc gga ttg aac cgc tgg atc ggc aaa gtg tat ttg ttg gtg tat gca	336
	Pro Gly Leu Asn Arg Trp Ile Gly Lys Val Tyr Leu Leu Val Tyr Ala	
	100 105 110	
20	ggc ttg tct tat gag cgt tgt tcc cgc aac cac aga cgt cat cac ctg	384
	Gly Leu Ser Tyr Glu Arg Cys Ser Arg Asn His Arg Arg His His Leu	
	115 120 125	
25	gca ccg gag acg ttc cag gat cct gac tac caa cgt tgc acc aat aac	432
	Ala Pro Glu Thr Phe Gln Asp Pro Asp Tyr Gln Arg Cys Thr Asn Asn	
	130 135 140	
30	aac atc cta gat tgg tat gtt cac ttc atg ggc aac tat ctg ggc atg	480
	Asn Ile Leu Asp Trp Tyr Val His Phe Met Gly Asn Tyr Leu Gly Met	
	145 150 155 160	
35	cgg caa ctg tta aat cta agc tgt ctt tgg ctg gcg cta atc att ctc	528
	Arg Gln Leu Leu Asn Leu Ser Cys Leu Trp Leu Ala Leu Ile Ile Leu	
	165 170 175	
40	aac ggt tct gat ctc cct gct cag atc atg cat ctg ctg ttg ttc agc	576
	Asn Gly Ser Asp Leu Pro Ala Gln Ile Met His Leu Leu Leu Phe Ser	
	180 185 190	
45	gtt ctg ccg ttg atc atc agt tcc tgt caa ttg ttt cta gtg gga acc	624
	Val Leu Pro Leu Ile Ile Ser Ser Cys Gln Leu Phe Leu Val Gly Thr	
	195 200 205	
50	tgg tta ccc cac cga cgt ggg gcc acg aca cga ccg ggc gtg aca acg	672
	Trp Leu Pro His Arg Arg Gly Ala Thr Thr Arg Pro Gly Val Thr Thr	
	210 215 220	

114

cgc agc ctg gct ttg cat cca gcc ctg tct ttc gca gct tgt tac aac 720  
 Arg Ser Leu Ala Leu His Pro Ala Leu Ser Phe Ala Ala Cys Tyr Asn  
 225 230 235 240

5 ttt ggc tat cat cgt gaa cat cat gaa tcg cct tcc aca ccc tgg ttt 768  
 Phe Gly Tyr His Arg Glu His His Glu Ser Pro Ser Thr Pro Trp Phe  
 245 250 255

10 cag ctg cca caa ctt cga aat gaa tca ttc act tga 804  
 Gln Leu Pro Gln Leu Arg Asn Glu Ser Phe Thr  
 260 265

15 <210> 86  
 <211> 267  
 <212> PRT

20 <213> Synechococcus WH8102

25 <400> 86  
 Met Lys Thr Thr Arg Ser Ile Ser Trp Pro Ser Thr Cys Trp His His  
 1 5 10 15

30 Gln Pro Ser Cys Ser Ser Trp Val Ala Asn Glu Phe Ser Pro Gln Ala  
 20 25 30

35 Leu Lys Gly Leu Ala Leu Ala Gly Leu Ile Gly Ser Ala Trp Leu Leu  
 35 40 45

40 Ser Leu Gly Leu Ser Tyr Thr Leu Pro Leu Asp Gln Thr Pro Gly Leu  
 50 55 60

45 Leu Ile Gly Ser Leu Ile Leu Leu Arg Ala Phe Leu His Thr Gly Leu  
 65 70 75 80

## 115

Phe Ile Val Ala His Asp Ser Met His Ala Ser Leu Val Pro Gly His  
 85 90 95

5 Pro Gly Leu Asn Arg Trp Ile Gly Lys Val Tyr Leu Leu Val Tyr Ala  
 100 105 110

10 Gly Leu Ser Tyr Glu Arg Cys Ser Arg Asn His Arg Arg His His Leu  
 115 120 125

15 Ala Pro Glu Thr Phe Gln Asp Pro Asp Tyr Gln Arg Cys Thr Asn Asn  
 130 135 140

Asn Ile Leu Asp Trp Tyr Val His Phe Met Gly Asn Tyr Leu Gly Met  
 145 150 155 160

20 Arg Gln Leu Leu Asn Leu Ser Cys Leu Trp Leu Ala Leu Ile Ile Leu  
 165 170 175

25 Asn Gly Ser Asp Leu Pro Ala Gln Ile Met His Leu Leu Leu Phe Ser  
 180 185 190

30 Val Leu Pro Leu Ile Ile Ser Ser Cys Gln Leu Phe Leu Val Gly Thr  
 195 200 205

35 Trp Leu Pro His Arg Arg Gly Ala Thr Thr Arg Pro Gly Val Thr Thr  
 210 215 220

40 Arg Ser Leu Ala Leu His Pro Ala Leu Ser Phe Ala Ala Cys Tyr Asn  
 225 230 235 240

45 Phe Gly Tyr His Arg Glu His His Glu Ser Pro Ser Thr Pro Trp Phe  
 245 250 255

Gln Leu Pro Gln Leu Arg Asn Glu Ser Phe Thr

260

265

5 <210> 87  
<211> 33  
<212> DNA  
10 <213> synthetic sequence  
  
<220>  
15 <221> primer\_bind  
<222> (1)..(33)  
20 <223>  
  
<400> 87  
25 gcattgctcta gacattataa agatattttg tga 33  
  
<210> 88  
30 <211> 33  
<212> DNA  
<213> synthetic sequence  
35  
  
<220>  
40 <221> primer\_bind  
<222> (1)..(33)  
  
<223>  
45



<400> 88  
 gcatgcatct agaaatgggt cagtgtcaac cat 33  
 5

<210> 89  
 <211> 805  
 10  
 <212> DNA  
 <213> Nostoc sp. Strain PCC7120  
 15

<220>  
 <221> variation  
 20  
 <222> (1)..(805)  
 <223>  
 25

<400> 89  
 gcatgcatct agaaatgggt cagtgtcaac catcatctct gcattcagaa aaactgggtg 60  
 30 tattgtcatc gacaatcaga gatgataaaa atattaataa gggatatattt attgcctgct 120  
 ttatcttatt tttatgggca attagtttaa tcttattact ctcaatagat acatccataa 180  
 ttcataagag cttattaggt atagccatgc tttggcagac cttcttatat acagggtttat 240  
 35 ttattactgc tcatgatgcc atgcacggcg tagtttatcc caaaaatccc agaataaata 300  
 attttatagg taagctcact ctaatcttgt atggactact cccttataaa gatttattga 360  
 40 aaaaacattg gttacaccac ggacatcctg gtactgattt agaccctgat tattacaatg 420  
 gtcacccca aaacttcttt ctttgggtatc tacattttat gaagtcttat tggcgatgga 480  
 cgcaaatttt cggattagtg atgatttttc atggacttaa aaatctggtg catataccag 540  
 45

118

aaaataattt aattatattt tggatgatac cttctatttt aagttcagta caactatttt 600  
at ttgtgttac at ttgtgcct cataaaaagc tagaagggtgg ttataactaac cccattgtg 660  
5 cgcgcagtat cccattacct cttttttggt cttttgttac ttgttatcac ttcggctacc 720  
acaaggaaca tcacgaatac cctcaacttc cttggtggaa attacctgaa gtcacaaaaa 780  
tatctttata aggtctagag catgc 805

10

&lt;210&gt; 90

&lt;211&gt; 35

15

&lt;212&gt; DNA

&lt;213&gt; synthetic sequence

20

&lt;220&gt;

&lt;221&gt; primer\_bind

25

&lt;222&gt; (1)..(35)

&lt;223&gt;

30

&lt;400&gt; 90

gagctcttca ttatttcgat ttgatttcg tgacc

35

35

&lt;210&gt; 91

&lt;211&gt; 44

40

&lt;212&gt; DNA

&lt;213&gt; synthetic sequence

45

<220>  
<221> primer\_bind  
5 <222> (1)..(44)  
<223>  
10  
<400> 91  
aagcttgagc tcggttgatc agaagaagaa gaagaagatg aact 44  
15 <210> 92  
<211> 653  
<212> DNA  
20 <213> Arabidopsis thaliana  
25 <220>  
<221> promoter  
<222> (1)..(653)  
30 <223>  
35 <400> 92  
gagctcttca ttatttcgat tttgatttcg tgaccagcga acgcagaata ccttgttgtg 60  
taatacttta cccgtgtaaa tcaaaaacaa aaaggctttt gagctttttg tagttgaatt 120  
40 tctctggctg atcttttctg tacagattca tatatctgca gagacgatat cattgattat 180  
ttgagcttct tttgaactat ttcgtgtaat ttgggatgag agctctatgt atgtgtgtaa 240  
actttgaaga caacaagaaa ggtaacaagt gagggagggg tgactccatg tcaaaataga 300  
45

120

tgtcataaga ggcccatcaa taagtgcttg agcccattag ctagcccagt aactaccaga 360  
ttgtgagatg gatgtgtgaa cagttttttt ttgatgtag gactgaaatg tgaacaacag 420  
5 gcgcatgaaa ggctaaatta ggacaatgat aagcagaaat aacttatcct ctctaact 480  
tggcctcaca ttgcccttca cacaatccac acacatccaa tcacaacctc atcatatc 540  
tcccgctaatt ctttttttct ttgatctttt tttttttgct tattattttt ttgactttga 600  
10 tctcccatca gttcatcttc ttcttcttct tctgatcaac cgagctcaag ctt 653

<210> 93  
15 <211> 28  
<212> DNA  
20 <213> synthetic sequence

<220>  
25 <221> primer\_bind  
<222> (1)..(28)

30 <223>

<400> 93  
35 gagctcactc actgatttcc attgcttg 28

<210> 94  
40 <211> 30  
<212> DNA  
<213> synthetic sequence  
45

<220>

5 <221> primer\_bind

<222> (1)..(30)

<223>

10

<400> 94

aagcttgagc tctttgttga agagatttgg

30

15

<210> 95

<211> 37

20

<212> DNA

<213> synthetic sequence

25

<220>

<221> primer\_bind

30

<222> (1)..(37)

<223>

35

<400> 95

cgccgttaag tcgatgtccg ttgatttaaa cagtgtc

37

40

<210> 96

<211> 34

<212> DNA

<213> synthetic sequence

5

<220>

<221> primer\_bind

10

<222> (1)..(34)

<223>

15

<400> 96

atcaacggac atcgacttaa cggcgtttgt aaac

34

20

<210> 97

<211> 831

25

<212> DNA

<213> *Haematococcus pluvialis*

30

<220>

<221> CDS

35

<222> (1)..(831)

<223>

40

<400> 97

atg cca tcc gag tcg tca gac gca gct cgt cct gtg ttg aag cac gcc  
Met Pro Ser Glu Ser Ser Asp Ala Ala Arg Pro Val Leu Lys His Ala

48

1

5

10

15

45

## 123

	tat aaa cct cca gca tct gac gcc aag ggc atc act atg gcg ctg acc	96
	Tyr Lys Pro Pro Ala Ser Asp Ala Lys Gly Ile Thr Met Ala Leu Thr	
	20 25 30	
5	atc att ggc acc tgg acc gca gtg ttt tta cac gca ata ttc caa atc	144
	Ile Ile Gly Thr Trp Thr Ala Val Phe Leu His Ala Ile Phe Gln Ile	
	35 40 45	
10	agg cta ccg aca tcc atg gac cag ctt cac tgg ttg cct gtg tcc gaa	192
	Arg Leu Pro Thr Ser Met Asp Gln Leu His Trp Leu Pro Val Ser Glu	
	50 55 60	
15	gcc aca gcc cag ctg ttg ggc gga agc agc agc cta ttg cac atc gcc	240
	Ala Thr Ala Gln Leu Leu Gly Gly Ser Ser Ser Leu Leu His Ile Ala	
	65 70 75 80	
20	gca gtc ttc att gta ctt gag ttt ctg tac act ggt cta ttc atc acc	288
	Ala Val Phe Ile Val Leu Glu Phe Leu Tyr Thr Gly Leu Phe Ile Thr	
	85 90 95	
25	acg cat gat gca atg cat ggc acc ata gct ttg agg aac agg cag ctc	336
	Thr His Asp Ala Met His Gly Thr Ile Ala Leu Arg Asn Arg Gln Leu	
	100 105 110	
30	aat gat ctc ctt ggc aac atc tgc ata tca ctg tac gcc tgg ttt gac	384
	Asn Asp Leu Leu Gly Asn Ile Cys Ile Ser Leu Tyr Ala Trp Phe Asp	
	115 120 125	
35	tac agc atg cac tgg gag cac cac aac cat act ggc gaa gtg ggg aaa	432
	Tyr Ser Met His Trp Glu His His Asn His Thr Gly Glu Val Gly Lys	
	130 135 140	
40	gac cct gac ttc cac aaa gga aat cct ggc ctt gtc ccc tgg ttc gcc	480
	Asp Pro Asp Phe His Lys Gly Asn Pro Gly Leu Val Pro Trp Phe Ala	
	145 150 155 160	
45	agc ttc atg tcc agc tac atg tcc ctg tgg cag ttt gcc cgg ctg gca	528
	Ser Phe Met Ser Ser Tyr Met Ser Leu Trp Gln Phe Ala Arg Leu Ala	
	165 170 175	
50	tgg tgg gca gtg gtg atg caa acg ttg ggg gcc ccc atg gcg aat ctc	576
	Trp Trp Ala Val Val Met Gln Thr Leu Gly Ala Pro Met Ala Asn Leu	
	180 185 190	
55	cta gtc ttc atg gct gca gcc cca atc ttg tca gca ttc cgc ctc ttc	624

124

Leu Val Phe Met Ala Ala Ala Pro Ile Leu Ser Ala Phe Arg Leu Phe  
 195 200 205

5    tac ttc ggc act tac ctg cca cac aag cct gag cca ggc cct gca gca    672  
      Tyr Phe Gly Thr Tyr Leu Pro His Lys Pro Glu Pro Gly Pro Ala Ala  
      210 215 220

10    ggc tct cag gtc atg tct tgg ttc agg gcc aag aca agt gag gca tct    720  
      Gly Ser Gln Val Met Ser Trp Phe Arg Ala Lys Thr Ser Glu Ala Ser  
      225 230 235 240

15    gat gtg atg agc ttc ctg aca tgc tac cac ttt gac ctg ttt gcc ccc    768  
      Asp Val Met Ser Phe Leu Thr Cys Tyr His Phe Asp Leu Phe Ala Pro  
      245 250 255

15    tgg tgg cag ctg ccc cac tgc cgc cgc ctg tct ggg cgt ggc ctg gtg    816  
      Trp Trp Gln Leu Pro His Cys Arg Arg Leu Ser Gly Arg Gly Leu Val  
      260 265 270

20    cct gcc ttg gca tga    831  
      Pro Ala Leu Ala  
      275

25    <210> 98  
      <211> 276  
      <212> PRT

30    <213> Haematococcus pluvialis

35    <400> 98  
      Met Pro Ser Glu Ser Ser Asp Ala Ala Arg Pro Val Leu Lys His Ala  
      1 5 10 15

40    Tyr Lys Pro Pro Ala Ser Asp Ala Lys Gly Ile Thr Met Ala Leu Thr  
      20 25 30

45    Ile Ile Gly Thr Trp Thr Ala Val Phe Leu His Ala Ile Phe Gln Ile



35

40

45

5 Arg Leu Pro Thr Ser Met Asp Gln Leu His Trp Leu Pro Val Ser Glu  
50 55 60

10 Ala Thr Ala Gln Leu Leu Gly Gly Ser Ser Ser Leu Leu His Ile Ala  
65 70 75 80

Ala Val Phe Ile Val Leu Glu Phe Leu Tyr Thr Gly Leu Phe Ile Thr  
85 90 95

15 Thr His Asp Ala Met His Gly Thr Ile Ala Leu Arg Asn Arg Gln Leu  
100 105 110

20 Asn Asp Leu Leu Gly Asn Ile Cys Ile Ser Leu Tyr Ala Trp Phe Asp  
115 120 125

25 Tyr Ser Met His Trp Glu His His Asn His Thr Gly Glu Val Gly Lys  
130 135 140

30 Asp Pro Asp Phe His Lys Gly Asn Pro Gly Leu Val Pro Trp Phe Ala  
145 150 155 160

Ser Phe Met Ser Ser Tyr Met Ser Leu Trp Gln Phe Ala Arg Leu Ala  
165 170 175

35 Trp Trp Ala Val Val Met Gln Thr Leu Gly Ala Pro Met Ala Asn Leu  
180 185 190

40 Leu Val Phe Met Ala Ala Ala Pro Ile Leu Ser Ala Phe Arg Leu Phe  
195 200 205

45 Tyr Phe Gly Thr Tyr Leu Pro His Lys Pro Glu Pro Gly Pro Ala Ala  
210 215 220

Gly Ser Gln Val Met Ser Trp Phe Arg Ala Lys Thr Ser Glu Ala Ser  
 225 230 235 240  
 5

Asp Val Met Ser Phe Leu Thr Cys Tyr His Phe Asp Leu Phe Ala Pro  
 245 250 255

10 Trp Trp Gln Leu Pro His Cys Arg Arg Leu Ser Gly Arg Gly Leu Val  
 260 265 270

15 Pro Ala Leu Ala  
 275

20 <210> 99  
 <211> 729  
 <212> DNA

25 <213> Paracoccus sp. MBIC1143

30 <220>  
 <221> CDS  
 <222> (1)..(729)

35 <223>

40 <400> 99  
 atg agc gca cat gcc ctg ccc aag gca gat ctg acc gcc acc agc ctg 48  
 Met Ser Ala His Ala Leu Pro Lys Ala Asp Leu Thr Ala Thr Ser Leu  
 1 5 10 15

45 atc gtc tcg ggc ggc atc atc gcc gct tgg ctg gcc ctg cat gtg cat 96  
 Ile Val Ser Gly Gly Ile Ile Ala Ala Trp Leu Ala Leu His Val His

	20	25	30	
5	gcg ctg tgg ttt ctg gac gca gcg gcg cat ccc atc ctg gcg atc gca Ala Leu Trp Phe Leu Asp Ala Ala Ala His Pro Ile Leu Ala Ile Ala	144		
	35	40	45	
10	aat ttc ctg ggg ctg acc tgg ctg tcg gtc gga ttg ttc atc atc gcg Asn Phe Leu Gly Leu Thr Trp Leu Ser Val Gly Leu Phe Ile Ile Ala	192		
	50	55	60	
15	cat gac gcg atg cac ggg tcg gtg gtg ccg ggg cgt ccg cgc gcc aat His Asp Ala Met His Gly Ser Val Val Pro Gly Arg Pro Arg Ala Asn	240		
	65	70	75	80
20	gcg gcg atg ggc cag ctt gtc ctg tgg ctg tat gcc gga ttt tcg tgg Ala Ala Met Gly Gln Leu Val Leu Trp Leu Tyr Ala Gly Phe Ser Trp	288		
	85	90	95	
25	cgc aag atg atc gtc aag cac atg gcc cat cac cgc cat gcc gga acc Arg Lys Met Ile Val Lys His Met Ala His His Arg His Ala Gly Thr	336		
	100	105	110	
30	gac gac gac ccc gat ttc gac cat ggc ggc ccg gtc cgc tgg tac gcc Asp Asp Asp Pro Asp Phe Asp His Gly Gly Pro Val Arg Trp Tyr Ala	384		
	115	120	125	
35	cgc ttc atc ggc acc tat ttc ggc tgg cgc gag ggg ctg ctg ctg ccc Arg Phe Ile Gly Thr Tyr Phe Gly Trp Arg Glu Gly Leu Leu Leu Pro	432		
	130	135	140	
40	gtc atc gtg acg gtc tat gcg ctg atc ctt ggg gat cgc tgg atg tac Val Ile Val Thr Val Tyr Ala Leu Ile Leu Gly Asp Arg Trp Met Tyr	480		
	145	150	155	160
45	gtg gtc ttc tgg ccg ctg ccg tcg atc ctg gcg tcg atc cag ctg ttc Val Val Phe Trp Pro Leu Pro Ser Ile Leu Ala Ser Ile Gln Leu Phe	528		
	165	170	175	
50	gtg ttc ggc acc tgg ctg ccg cac cgc ccc ggc cac gac gcg ttc ccg Val Phe Gly Thr Trp Leu Pro His Arg Pro Gly His Asp Ala Phe Pro	576		
	180	185	190	
55	gac cgc cac aat gcg cgg tcg tcg cgg atc agc gac ccc gtg tcg ctg Asp Arg His Asn Ala Arg Ser Ser Arg Ile Ser Asp Pro Val Ser Leu	624		
	195	200	205	

ctg acc tgc ttt cac ttt ggc ggt tat tat cac gaa cac cac ctg cac 672  
 Leu Thr Cys Phe His Phe Gly Gly Tyr His His Glu His His Leu His  
 210 215 220

5

ccg acg gtg ccg tgg tgg cgc ctg ccc agc acc cgc acc aag ggg gac 720  
 Pro Thr Val Pro Trp Trp Arg Leu Pro Ser Thr Arg Thr Lys Gly Asp  
 225 230 235 240

10

acc gca tga 729  
 Thr Ala

15

<210> 100  
 <211> 242  
 <212> PRT

20

<213> Paracoccus sp. MBIC1143

25

<400> 100  
 Met Ser Ala His Ala Leu Pro Lys Ala Asp Leu Thr Ala Thr Ser Leu  
 1 5 10 15

30

Ile Val Ser Gly Gly Ile Ile Ala Ala Trp Leu Ala Leu His Val His  
 20 25 30

35

Ala Leu Trp Phe Leu Asp Ala Ala Ala His Pro Ile Leu Ala Ile Ala  
 35 40 45

40

Asn Phe Leu Gly Leu Thr Trp Leu Ser Val Gly Leu Phe Ile Ile Ala  
 50 55 60

45

His Asp Ala Met His Gly Ser Val Val Pro Gly Arg Pro Arg Ala Asn  
 65 70 75 80

Ala Ala, Met Gly Gln Leu Val Leu Trp Leu Tyr Ala Gly Phe Ser Trp  
 85 90 95

5

Arg Lys Met Ile Val Lys His Met Ala His His Arg His Ala Gly Thr  
 100 105 110

10

Asp Asp Asp Pro Asp Phe Asp His Gly Gly Pro Val Arg Trp Tyr Ala  
 115 120 125

15

Arg Phe Ile Gly Thr Tyr Phe Gly Trp Arg Glu Gly Leu Leu Leu Pro  
 130 135 140

20

Val Ile Val Thr Val Tyr Ala Leu Ile Leu Gly Asp Arg Trp Met Tyr  
 145 150 155 160

Val Val Phe Trp Pro Leu Pro Ser Ile Leu Ala Ser Ile Gln Leu Phe  
 165 170 175

25

Val Phe Gly Thr Trp Leu Pro His Arg Pro Gly His Asp Ala Phe Pro  
 180 185 190

30

Asp Arg His Asn Ala Arg Ser Ser Arg Ile Ser Asp Pro Val Ser Leu  
 195 200 205

35

Leu Thr Cys Phe His Phe Gly Gly Tyr His His Glu His His Leu His  
 210 215 220

40

Pro Thr Val Pro Trp Trp Arg Leu Pro Ser Thr Arg Thr Lys Gly Asp  
 225 230 235 240

Thr Ala

45

&lt;210&gt; 101

&lt;211&gt; 735

5 &lt;212&gt; DNA

&lt;213&gt; Brevundimonas aurantiaca

10

&lt;220&gt;

&lt;221&gt; CDS

15 &lt;222&gt; (1)..(735)

&lt;223&gt;

20

&lt;400&gt; 101

atg acc gcc gcc gtc gcc gag cca cgc acc gtc ccg cgc cag acc tgg 48  
 Met Thr Ala Ala Val Ala Glu Pro Arg Thr Val Pro Arg Gln Thr Trp  
 1 5 10 15

25

atc ggt ctg acc ctg gcg gga atg atc gtg gcg gga tgg gcg gtt ctg 96  
 Ile Gly Leu Thr Leu Ala Gly Met Ile Val Ala Gly Trp Ala Val Leu  
 20 25 30

30

cat gtc tac ggc gtc tat ttt cac cga tgg ggg ccg ttg acc ctg gtg 144  
 His Val Tyr Gly Val Tyr Phe His Arg Trp Gly Pro Leu Thr Leu Val  
 35 40 45

35

atc gcc ccg gcg atc gtg gcg gtc cag acc tgg ttg tcg gtc ggc ctt 192  
 Ile Ala Pro Ala Ile Val Ala Val Gln Thr Trp Leu Ser Val Gly Leu  
 50 55 60

40

ttc atc gtc gcc cat gac gcc atg tac ggc tcc ctg gcg ccg gga cgg 240  
 Phe Ile Val Ala His Asp Ala Met Tyr Gly Ser Leu Ala Pro Gly Arg  
 65 70 75 80

ccg cgg ctg aac gcc gca gtc ggc cgg ctg acc ctg ggg ctc tat gcg 288  
 Pro Arg Leu Asn Ala Ala Val Gly Arg Leu Thr Leu Gly Leu Tyr Ala  
 85 90 95

45

## 131

ggc ttc cgc ttc gat cgg ctg aag acg gcg cac cac gcc cac cac gcc 336  
 Gly Phe, Arg Phe Asp Arg Leu Lys Thr Ala His His Ala His His Ala  
 100 105 110

5 gcg ccc ggc acg gcc gac gac ccg gat ttt cac gcc ccg gcg ccc cgc 384  
 Ala Pro Gly Thr Ala Asp Asp Pro Asp Phe His Ala Pro Ala Pro Arg  
 115 120 125

10 gcc ttc ctt ccc tgg ttc ctg aac ttc ttt cgc acc tat ttc ggc tgg 432  
 Ala Phe Leu Pro Trp Phe Leu Asn Phe Phe Arg Thr Tyr Phe Gly Trp  
 130 135 140

15 cgc gag atg gcg gtc ctg acc gcc ctg gtc ctg atc gcc ctc ttc ggc 480  
 Arg Glu Met Ala Val Leu Thr Ala Leu Val Leu Ile Ala Leu Phe Gly  
 145 150 155 160

20 ctg ggg gcg cgg ccg gcc aat ctc ctg acc ttc tgg gcc gcg ccg gcc 528  
 Leu Gly Ala Arg Pro Ala Asn Leu Leu Thr Phe Trp Ala Ala Pro Ala  
 165 170 175

ctg ctt tca gcg ctt cag ctc ttc acc ttc ggc acc tgg ctg ccg cac 576  
 Leu Leu Ser Ala Leu Gln Leu Phe Thr Phe Gly Thr Trp Leu Pro His  
 180 185 190

25 cgc cac acc gac cag ccg ttc gcc gac gcg cac cac gcc cgc agc agc 624  
 Arg His Thr Asp Gln Pro Phe Ala Asp Ala His His Ala Arg Ser Ser  
 195 200 205

30 ggc tac ggc ccc gtg ctt tcc ctg ctc acc tgt ttc cac ttc ggc cgc 672  
 Gly Tyr Gly Pro Val Leu Ser Leu Leu Thr Cys Phe His Phe Gly Arg  
 210 215 220

35 cac cac gaa cac cat ctg agc ccc tgg cgg ccc tgg tgg cgt ctg tgg 720  
 His His Glu His His Leu Ser Pro Trp Arg Pro Trp Trp Arg Leu Trp  
 225 230 235 240

cgc ggc gag tct tga 735  
 Arg Gly Glu Ser

40

&lt;210&gt; 102

&lt;211&gt; 244

45

&lt;212&gt; PRT

&lt;213&gt; Brevundimonas aurantiaca

5

&lt;400&gt; 102

Met Thr Ala Ala Val Ala Glu Pro Arg Thr Val Pro Arg Gln Thr Trp  
 10 1 5 10 15

Ile Gly Leu Thr Leu Ala Gly Met Ile Val Ala Gly Trp Ala Val Leu  
 20 25 30

15

His Val Tyr Gly Val Tyr Phe His Arg Trp Gly Pro Leu Thr Leu Val  
 35 40 45

20

Ile Ala Pro Ala Ile Val Ala Val Gln Thr Trp Leu Ser Val Gly Leu  
 50 55 60

Phe Ile Val Ala His Asp Ala Met Tyr Gly Ser Leu Ala Pro Gly Arg  
 65 70 75 80

Pro Arg Leu Asn Ala Ala Val Gly Arg Leu Thr Leu Gly Leu Tyr Ala  
 85 90 95

30

Gly Phe Arg Phe Asp Arg Leu Lys Thr Ala His His Ala His His Ala  
 100 105 110

35

Ala Pro Gly Thr Ala Asp Asp Pro Asp Phe His Ala Pro Ala Pro Arg  
 115 120 125

40

Ala Phe Leu Pro Trp Phe Leu Asn Phe Phe Arg Thr Tyr Phe Gly Trp  
 130 135 140

45 Arg Glu Met Ala Val Leu Thr Ala Leu Val Leu Ile Ala Leu Phe Gly



133

145                      150                      155                      160

Leu Gly Ala Arg Pro Ala Asn Leu Leu Thr Phe Trp Ala Ala Pro Ala  
5                      165                      170                      175

Leu Leu Ser Ala Leu Gln Leu Phe Thr Phe Gly Thr Trp Leu Pro His  
10                      180                      185                      190

Arg His Thr Asp Gln Pro Phe Ala Asp Ala His His Ala Arg Ser Ser  
15                      195                      200                      205

Gly Tyr Gly Pro Val Leu Ser Leu Leu Thr Cys Phe His Phe Gly Arg  
210                      215                      220

His His Glu His His Leu Ser Pro Trp Arg Pro Trp Trp Arg Leu Trp  
20                      225                      230                      235                      240

Arg Gly Glu Ser  
25

<210> 103

30 <211> 690

"  
<212> DNA

"  
<213> Nodularia spumigena NSOR10  
35

<220>

40 <221> CDS

<222> (1)..(690)

<223>  
45

<400> 103

5 atg gcg atc gcc att att agt ata tgg gct atc agc cta ggt ttg tta 48  
Met Ala Ile Ala Ile Ile Ser Ile Trp Ala Ile Ser Leu Gly Leu Leu  
1 5 10 15

10 ctt tat att gat ata tcc caa ttc aag ttt tgg atg ttg tta ccg ctc 96  
Leu Tyr Ile Asp Ile Ser Gln Phe Lys Phe Trp Met Leu Leu Pro Leu  
20 25 30

15 ata ttt tgg caa aca ttt tta tat acg gga tta ttt att aca gct cat 144  
Ile Phe Trp Gln Thr Phe Leu Tyr Thr Gly Leu Phe Ile Thr Ala His  
35 40 45

gat gcc atg cat ggg gta gtt ttt ccc aaa aat ccc aaa atc aac cat 192  
Asp Ala Met His Gly Val Val Phe Pro Lys Asn Pro Lys Ile Asn His  
50 55 60

20 ttc att ggc tca ttg tgc ctg ttt ctt tat ggt ctt tta cct tat caa 240  
Phe Ile Gly Ser Leu Cys Leu Phe Leu Tyr Gly Leu Leu Pro Tyr Gln  
65 70 75 80

25 aaa ctt tta aaa aag cat tgg cta cat cac cat aat cca gcc agt gaa 288  
Lys Leu Leu Lys Lys His Trp Leu His His His Asn Pro Ala Ser Glu  
85 90 95

30 aca gat cca gat ttt cac aac ggg aag cag aaa aac ttt ttt gct tgg 336  
Thr Asp Pro Asp Phe His Asn Gly Lys Gln Lys Asn Phe Phe Ala Trp  
100 105 110

35 tat tta tat ttt atg aag cgt tac tgg agt tgg tta caa att atc aca 384  
Tyr Leu Tyr Phe Met Lys Arg Tyr Trp Ser Trp Leu Gln Ile Ile Thr  
115 120 125

tta atg att att tat aac tta cta aaa tat ata tgg cat ttt cca gag 432  
Leu Met Ile Ile Tyr Asn Leu Leu Lys Tyr Ile Trp His Phe Pro Glu  
130 135 140

40 gat aat atg act tat ttt tgg gta gtt ccc tca att tta agt tct tta 480  
Asp Asn Met Thr Tyr Phe Trp Val Val Pro Ser Ile Leu Ser Ser Leu  
145 150 155 160

45 caa tta ttt tat ttt gga act ttt cta ccc cac agt gag cct gta gaa 528  
Gln Leu Phe Tyr Phe Gly Thr Phe Leu Pro His Ser Glu Pro Val Glu

135

165

170

175

5 ggt tat aaa gag cct cat cgt tcc caa act att agc cgt ccc att tgg 576  
 Gly Tyr Lys Glu Pro His Arg Ser Gln Thr Ile Ser Arg Pro Ile Trp  
 180 185 190

10 tgg tca ttt ata act tgt tac cat ttt ggt tat cat tac gaa cat cat 624  
 Trp Ser Phe Ile Thr Cys Tyr His Phe Gly Tyr His Tyr Glu His His  
 195 200 205

gaa tac ccc cat gtt cct tgg tgg caa tta cca gaa att tat aaa atg 672  
 Glu Tyr Pro His Val Pro Trp Trp Gln Leu Pro Glu Ile Tyr Lys Met  
 210 215 220

15 tct aaa tca aat ttg tga 690  
 Ser Lys Ser Asn Leu  
 225

20 <210> 104  
 <211> 229  
 <212> PRT

25 <213> Nodularia spumigena NSOR10

30 <400> 104  
 Met Ala Ile Ala Ile Ile Ser Ile Trp Ala Ile Ser Leu Gly Leu Leu  
 1 5 10 15

35 Leu Tyr Ile Asp Ile Ser Gln Phe Lys Phe Trp Met Leu Leu Pro Leu  
 20 25 30

40 Ile Phe Trp Gln Thr Phe Leu Tyr Thr Gly Leu Phe Ile Thr Ala His  
 35 40 45

45 Asp Ala Met His Gly Val Val Phe Pro Lys Asn Pro Lys Ile Asn His  
 50 55 60

Phe Ile Gly Ser Leu Cys Leu Phe Leu Tyr Gly Leu Leu Pro Tyr Gln  
 65 70 75 80  
 5

Lys Leu Leu Lys Lys His Trp Leu His His His Asn Pro Ala Ser Glu  
 85 90 95

10  
 Thr Asp Pro Asp Phe His Asn Gly Lys Gln Lys Asn Phe Phe Ala Trp  
 100 105 110

15  
 Tyr Leu Tyr Phe Met Lys Arg Tyr Trp Ser Trp Leu Gln Ile Ile Thr  
 115 120 125

20  
 Leu Met Ile Ile Tyr Asn Leu Leu Lys Tyr Ile Trp His Phe Pro Glu  
 130 135 140

25  
 Asp Asn Met Thr Tyr Phe Trp Val Val Pro Ser Ile Leu Ser Ser Leu  
 145 150 155 160

30  
 Gln Leu Phe Tyr Phe Gly Thr Phe Leu Pro His Ser Glu Pro Val Glu  
 165 170 175

35  
 Gly Tyr Lys Glu Pro His Arg Ser Gln Thr Ile Ser Arg Pro Ile Trp  
 180 185 190

40  
 Trp Ser Phe Ile Thr Cys Tyr His Phe Gly Tyr His Tyr Glu His His  
 195 200 205

45  
 Glu Tyr Pro His Val Pro Trp Trp Gln Leu Pro Glu Ile Tyr Lys Met  
 210 215 220

Ser Lys Ser Asn Leu  
 225

&lt;210&gt; 105

&lt;211&gt; 1536

5

&lt;212&gt; DNA

&lt;213&gt; Deinococcus radiodurans R1

10

&lt;220&gt;

&lt;221&gt; CDS

15

&lt;222&gt; (1)..(1536)

&lt;223&gt;

20

&lt;400&gt; 105

atg ccg gat tac gac ctg atc gtc atg ggc gcg ggc cac aac gcg ctg 48

Met Pro Asp Tyr Asp Leu Ile Val Met Gly Ala Gly His Asn Ala Leu

25

1

5

10

15

gtg act gct gcc tac gcc gcc cgg gcg ggc ctg aaa gtc ggc gtg ttc 96

Val Thr Ala Ala Tyr Ala Ala Arg Ala Gly Leu Lys Val Gly Val Phe

20

25

30

30

gag cgg cgg gac ctc gtc ggc ggg gcg gtc agc acc gag gag gtc gtg 144

Glu Arg Arg His Leu Val Gly Gly Ala Val Ser Thr Glu Glu Val Val

35

40

45

35

ccc ggt tac cgc ttc gac tac ggc ggc agc gcc cac atc ctg att cgg 192

Pro Gly Tyr Arg Phe Asp Tyr Gly Gly Ser Ala His Ile Leu Ile Arg

50

55

60

40

atg acg ccc atc gtg cgc gaa ctc gaa ctc acg cgg cac ggg ctg cat 240

Met Thr Pro Ile Val Arg Glu Leu Glu Leu Thr Arg His Gly Leu His

65

70

75

80

tac ctc gaa gtg gac cct atg ttt cac gct tcc gac ggt gaa acg ccc 288

Tyr Leu Glu Val Asp Pro Met Phe His Ala Ser Asp Gly Glu Thr Pro

45

85

90

95

	tgg ttc, att cac cgc gac gcc ggg cgg acc atc cgc gaa ctg gac gaa	336
	Trp Phe Ile His Arg Asp Ala Gly Arg Thr Ile Arg Glu Leu Asp Glu	
	100 105 110	
5	aag ttt ccc ggg cag ggc gac gcc tac ggg cgc ttt ctc gac gat tgg	384
	Lys Phe Pro Gly Gln Gly Asp Ala Tyr Gly Arg Phe Leu Asp Asp Trp	
	115 120 125	
10	aca ccc ttc gcg cgc gcc gtg gcc gac ctg ttc aac tcg gcg ccg ggg	432
	Thr Pro Phe Ala Arg Ala Val Ala Asp Leu Phe Asn Ser Ala Pro Gly	
	130 135 140	
	ccg ctc gac ctg ggc aaa atg gtg atg cgc agc ggc cag ggc aag gac	480
15	Pro Leu Asp Leu Gly Lys Met Val Met Arg Ser Gly Gln Gly Lys Asp	
	145 150 155 160	
	tgg aac gag cag ctc ccg cgc atc ctg cgg ccc tac ggc gac gtg gcg	528
20	Trp Asn Glu Gln Leu Pro Arg Ile Leu Arg Pro Tyr Gly Asp Val Ala	
	165 170 175	
	cgc gag tac ttc agc gag gag cgc gtg cgg gct ccc ctg acc tgg atg	576
	Arg Glu Tyr Phe Ser Glu Glu Arg Val Arg Ala Pro Leu Thr Trp Met	
	180 185 190	
25	gcg gcc cag agc ggc ccc cca ccc tcg gac ccg ctg agc gcg ccc ttt	624
	Ala Ala Gln Ser Gly Pro Pro Ser Asp Pro Leu Ser Ala Pro Phe	
	195 200 205	
30	ttg ctg tgg cac ccg ctc tac cac gaa ggc ggc gtg gcg cgg ccc aaa	672
	Leu Leu Trp His Pro Leu Tyr His Glu Gly Gly Val Ala Arg Pro Lys	
	210 215 220	
	ggc ggc agc ggc ggc ctg acc aaa gcc ctg cgc cgg gcc acc gag gcc	720
35	Gly Gly Ser Gly Gly Leu Thr Lys Ala Leu Arg Arg Ala Thr Glu Ala	
	225 230 235 240	
	gaa ggc ggc gag gtc ttc acc gac gcg ccg gtc aag gaa att ctg gtc	768
40	Glu Gly Gly Glu Val Phe Thr Asp Ala Pro Val Lys Glu Ile Leu Val	
	245 250 255	
	aag gac ggc aag gcg cag ggc atc cgg ctg gaa agc ggc gag acg tac	816
	Lys Asp Gly Lys Ala Gln Gly Ile Arg Leu Glu Ser Gly Glu Thr Tyr	
	260 265 270	
45		

139

	acc gcc cgc gcc gtc gtg tgc ggc gtc cac atc ctg acc act gcg aat	864
	Thr Ala Arg Ala Val Val Ser Gly Val His Ile Leu Thr Thr Ala Asn	
	275 280 285	
5	gcc ctg ccc gcc gaa tat gtc cct agc gcc gcc agg aat gtg cgc gtg	912
	Ala Leu Pro Ala Glu Tyr Val Pro Ser Ala Ala Arg Asn Val Arg Val	
	290 295 300	
10	ggc aac ggc ttc ggc atg att ttg cgc ctc gcc ctc agt gaa aaa gtc	960
	Gly Asn Gly Phe Gly Met Ile Leu Arg Leu Ala Leu Ser Glu Lys Val	
	305 310 315 320	
15	aaa tac cgt cac cac acc gag ccc gac tca cgc atc ggc ctg gga ttg	1008
	Lys Tyr Arg His His Thr Glu Pro Asp Ser Arg Ile Gly Leu Gly Leu	
	325 330 335	
20	ctg atc aaa aac gag cgg caa atc atg cag ggc tac ggc gaa tac ctc	1056
	Leu Ile Lys Asn Glu Arg Gln Ile Met Gln Gly Tyr Gly Glu Tyr Leu	
	340 345 350	
	gcc ggg cag ccc atc acc gac ccg ccc ctc gtc gcc atg agc ttc agc	1104
	Ala Gly Gln Pro Thr Thr Asp Pro Pro Leu Val Ala Met Ser Phe Ser	
	355 360 365	
25	gcg gtg gac gac tgc ctc gcc cca ccg aac ggc gac gtg ttg tgg ctg	1152
	Ala Val Asp Asp Ser Leu Ala Pro Pro Asn Gly Asp Val Leu Trp Leu	
	370 375 380	
30	tgg gcg cag tac tac ccc ttc gag ctc gcc acc ggg agc tgg gaa acg	1200
	Trp Ala Gln Tyr Tyr Pro Phe Glu Leu Ala Thr Gly Ser Trp Glu Thr	
	385 390 395 400	
35	cgc acc gcc gaa gcg cgg gag aac atc ctg cgg gcc ttt gag cac tac	1248
	Arg Thr Ala Glu Ala Arg Glu Asn Ile Leu Arg Ala Phe Glu His Tyr	
	405 410 415	
40	gcg ccg ggc acc cgc gac acg att gtg ggc gaa ctc gtg cag acg ccg	1296
	Ala Pro Gly Thr Arg Asp Thr Ile Val Gly Glu Leu Val Gln Thr Pro	
	420 425 430	
	cag tgg ctg gaa acc aac ctc ggc ctg cac cgg ggc aac gtg atg cac	1344
	Gln Trp Leu Glu Thr Asn Leu Gly Leu His Arg Gly Asn Val Met His	
	435 440 445	
45	ctg gaa atg tcc ttc gac cag atg ttc tcc ttc cgc ccc tgg ctg aaa	1392

140

	Leu	Glu	Met	Ser	Phe	Asp	Gln	Met	Phe	Ser	Phe	Arg	Pro	Trp	Leu	Lys	
	450,						455					460					
	gcg	agc	cag	tac	cgc	tgg	ccg	ggc	gtg	cag	ggg	ctg	tac	ctc	acc	ggc	1440
5	Ala	Ser	Gln	Tyr	Arg	Trp	Pro	Gly	Val	Gln	Gly	Leu	Tyr	Leu	Thr	Gly	
	465					470					475					480	
	gcc	agc	acc	cac	ccc	ggc	gga	ggc	atc	atg	ggc	gcc	tcg	gga	cgc	aac	1488
10	Ala	Ser	Thr	His	Pro	Gly	Gly	Gly	Ile	Met	Gly	Ala	Ser	Gly	Arg	Asn	
				485						490					495		
	gcg	gcg	cgg	gtc	atc	gtg	aag	gac	ctg	acg	cgg	agg	cgc	tgg	aaa	tga	1536
	Ala	Ala	Arg	Val	Ile	Val	Lys	Asp	Leu	Thr	Arg	Arg	Arg	Trp	Lys		
				500					505					510			
15																	
	<210>	106															
	<211>	511															
20	<212>	PRT															
	<213>	Deinococcus radiodurans R1															
25																	
	<400>	106															
	Met	Pro	Asp	Tyr	Asp	Leu	Ile	Val	Met	Gly	Ala	Gly	His	Asn	Ala	Leu	
30	1				5					10					15		
	Val	Thr	Ala	Ala	Tyr	Ala	Ala	Arg	Ala	Gly	Leu	Lys	Val	Gly	Val	Phe	
				20					25					30			
35																	
	Glu	Arg	Arg	His	Leu	Val	Gly	Gly	Ala	Val	Ser	Thr	Glu	Glu	Val	Val	
				35				40						45			
40																	
	Pro	Gly	Tyr	Arg	Phe	Asp	Tyr	Gly	Gly	Ser	Ala	His	Ile	Leu	Ile	Arg	
	50							55					60				
45	Met	Thr	Pro	Ile	Val	Arg	Glu	Leu	Glu	Leu	Thr	Arg	His	Gly	Leu	His	



65		70		75		80										
5	Tyr	Leu	Glu	Val	Asp	Pro	Met	Phe	His	Ala	Ser	Asp	Gly	Glu	Thr	Pro
				85						90					95	
10	Trp	Phe	Ile	His	Arg	Asp	Ala	Gly	Arg	Thr	Ile	Arg	Glu	Leu	Asp	Glu
				100					105					110		
15	Lys	Phe	Pro	Gly	Gln	Gly	Asp	Ala	Tyr	Gly	Arg	Phe	Leu	Asp	Asp	Trp
			115					120						125		
20	Thr	Pro	Phe	Ala	Arg	Ala	Val	Ala	Asp	Leu	Phe	Asn	Ser	Ala	Pro	Gly
			130					135					140			
25	Pro	Leu	Asp	Leu	Gly	Lys	Met	Val	Met	Arg	Ser	Gly	Gln	Gly	Lys	Asp
			145				150				155				160	
30	Trp	Asn	Glu	Gln	Leu	Pro	Arg	Ile	Leu	Arg	Pro	Tyr	Gly	Asp	Val	Ala
					165					170					175	
35	Arg	Glu	Tyr	Phe	Ser	Glu	Glu	Arg	Val	Arg	Ala	Pro	Leu	Thr	Trp	Met
				180					185						190	
40	Ala	Ala	Gln	Ser	Gly	Pro	Pro	Pro	Ser	Asp	Pro	Leu	Ser	Ala	Pro	Phe
			195						200					205		
45	Leu	Leu	Trp	His	Pro	Leu	Tyr	His	Glu	Gly	Gly	Val	Ala	Arg	Pro	Lys
			210					215						220		
50	Gly	Gly	Ser	Gly	Gly	Leu	Thr	Lys	Ala	Leu	Arg	Arg	Ala	Thr	Glu	Ala
			225					230				235			240	
55	Glu	Gly	Gly	Glu	Val	Phe	Thr	Asp	Ala	Pro	Val	Lys	Glu	Ile	Leu	Val
					245					250					255	

Lys Asp Gly Lys Ala Gln Gly Ile Arg Leu Glu Ser Gly Glu Thr Tyr  
 260 265 270  
 5  
 Thr Ala Arg Ala Val Val Ser Gly Val His Ile Leu Thr Thr Ala Asn  
 275 280 285  
 10  
 Ala Leu Pro Ala Glu Tyr Val Pro Ser Ala Ala Arg Asn Val Arg Val  
 290 295 300  
 15  
 Gly Asn Gly Phe Gly Met Ile Leu Arg Leu Ala Leu Ser Glu Lys Val  
 305 310 315 320  
 20  
 Lys Tyr Arg His His Thr Glu Pro Asp Ser Arg Ile Gly Leu Gly Leu  
 325 330 335  
 25  
 Leu Ile Lys Asn Glu Arg Gln Ile Met Gln Gly Tyr Gly Glu Tyr Leu  
 340 345 350  
 30  
 Ala Gly Gln Pro Thr Thr Asp Pro Pro Leu Val Ala Met Ser Phe Ser  
 355 360 365  
 35  
 Trp Ala Gln Tyr Tyr Pro Phe Glu Leu Ala Thr Gly Ser Trp Glu Thr  
 385 390 395 400  
 40  
 Arg Thr Ala Glu Ala Arg Glu Asn Ile Leu Arg Ala Phe Glu His Tyr  
 405 410 415  
 45  
 Ala Pro Gly Thr Arg Asp Thr Ile Val Gly Glu Leu Val Gln Thr Pro  
 420 425 430

143

Gln Trp Leu Glu Thr Asn Leu Gly Leu His Arg Gly Asn Val Met His  
 435 440 445

5

Leu Glu Met Ser Phe Asp Gln Met Phe Ser Phe Arg Pro Trp Leu Lys  
 450 455 460

10

Ala Ser Gln Tyr Arg Trp Pro Gly Val Gln Gly Leu Tyr Leu Thr Gly  
 465 470 475 480

15

Ala Ser Thr His Pro Gly Gly Gly Ile Met Gly Ala Ser Gly Arg Asn  
 485 490 495

20

Ala Ala Arg Val Ile Val Lys Asp Leu Thr Arg Arg Arg Trp Lys  
 500 505 510

&lt;210&gt; 107

&lt;211&gt; 1666

25

&lt;212&gt; DNA

&lt;213&gt; Lycopersicon esculentum

30

&lt;220&gt;

&lt;221&gt; CDS

35

&lt;222&gt; (1)..(1494)

&lt;223&gt;

40

&lt;400&gt; 107

atg gaa gct ctt ctc aag cct ttt cca tct ctt tta ctt tcc tct cct  
 Met Glu Ala Leu Leu Lys Pro Phe Pro Ser Leu Leu Leu Ser Ser Pro

48

45

1

5

10

15

	pca ccc cat agg tct att ttc caa caa aat ccc tct ttt cta agt ccc	96
	Thr Pro His Arg Ser Ile Phe Gln Gln Asn Pro Ser Phe Leu Ser Pro	
	20 25 30	
5	acc acc aaa aaa aaa tca aga aaa tgt ctt ctt aga aac aaa agt agt	144
	Thr Thr Lys Lys Lys Ser Arg Lys Cys Leu Leu Arg Asn Lys Ser Ser	
	35 40 45	
10	aaa ctt ttt tgt agc ttt ctt gat tta gca ccc aca tca aag cca gag	192
	Lys Leu Phe Cys Ser Phe Leu Asp Leu Ala Pro Thr Ser Lys Pro Glu	
	50 55 60	
15	tct tta gat gtt aac atc tca tgg gtt gat cct aat tcg aat cgg gct	240
	Ser Leu Asp Val Asn Ile Ser Trp Val Asp Pro Asn Ser Asn Arg Ala	
	65 70 75 80	
20	caa ttc gac gtg atc att atc gga gct ggc cct gct ggg ctc agg cta	288
	Gln Phe Asp Val Ile Ile Ile Gly Ala Gly Pro Ala Gly Leu Arg Leu	
	85 90 95	
25	gct gaa caa gtt tct aaa tat ggt att aag gta tgt tgt gtt gac cct	336
	Ala Glu Gln Val Ser Lys Tyr Gly Ile Lys Val Cys Cys Val Asp Pro	
	100 105 110	
30	tca cca ctc tcc atg tgg cca aat aat tat ggt gtt tgg gtt gat gag	384
	Ser Pro Leu Ser Met Trp Pro Asn Asn Tyr Gly Val Trp Val Asp Glu	
	115 120 125	
35	ttt gag aat tta gga ctg gaa aat tgt tta gat cat aaa tgg cct atg	432
	Phe Glu Asn Leu Gly Leu Glu Asn Cys Leu Asp His Lys Trp Pro Met	
	130 135 140	
40	act tgt gtg cat ata aat gat aac aaa act aag tat ttg gga aga cca	480
	Thr Cys Val His Ile Asn Asp Asn Lys Thr Lys Tyr Leu Gly Arg Pro	
	145 150 155 160	
45	tat ggt aga gtt agt aga aag aag ctg aag ttg aaa ttg ttg aat agt	528
	Tyr Gly Arg Val Ser Arg Lys Lys Leu Lys Leu Lys Leu Leu Asn Ser	
	165 170 175	
50	tgt gtt gag aac aga gtg aag ttt tat aaa gct aag gtt tgg aaa gtg	576
	Cys Val Glu Asn Arg Val Lys Phe Tyr Lys Ala Lys Val Trp Lys Val	
	180 185 190	

145

	gaa cat gaa gaa ttt gag tct tca att gtt tgt gat gat ggt aag aag	624
	Glu His Glu Glu Phe Glu Ser Ser Ile Val Cys Asp Asp Gly Lys Lys	
	195 200 205	
5	ata aga ggt agt ttg gtt gtg gat gca agt ggt ttt gct agt gat ttt	672
	Ile Arg Gly Ser Leu Val Val Asp Ala Ser Gly Phe Ala Ser Asp Phe	
	210 215 220	
10	ata gag tat gac agg cca aga aac cat ggt tat caa att gct cat ggg	720
	Ile Glu Tyr Asp Arg Pro Arg Asn His Gly Tyr Gln Ile Ala His Gly	
	225 230 235 240	
15	gtt tta gta gaa gtt gat aat cat cca ttt gat ttg gat aaa atg gtg	768
	Val Leu Val Glu Val Asp Asn His Pro Phe Asp Leu Asp Lys Met Val	
	245 250 255	
20	ctt atg gat tgg agg gat tct cat ttg ggt aat gag cca tat tta agg	816
	Leu Met Asp Trp Arg Asp Ser His Leu Gly Asn Glu Pro Tyr Leu Arg	
	260 265 270	
25	gtg aat aat gct aaa gaa cca aca ttc ttg tat gca atg cca ttt gat	864
	Val Asn Asn Ala Lys Glu Pro Thr Phe Leu Tyr Ala Met Pro Phe Asp	
	275 280 285	
30	aga gat ttg gtt ttc ttg gaa gag act tct ttg gtg agt cgt cct gtt	912
	Arg Asp Leu Val Phe Leu Glu Glu Thr Ser Leu Val Ser Arg Pro Val	
	290 295 300	
35	tta tcg tat atg gaa gta aaa aga agg atg gtg gca aga tta agg cat	960
	Leu Ser Tyr Met Glu Val Lys Arg Arg Met Val Ala Arg Leu Arg His	
	305 310 315 320	
40	ttg ggg atc aaa gtg aaa agt gtt att gag gaa gag aaa tgt gtg atc	1008
	Leu Gly Ile Lys Val Lys Ser Val Ile Glu Glu Glu Lys Cys Val Ile	
	325 330 335	
45	cct atg gga gga cca ctt ccg cgg att cct caa aat gtt atg gct att	1056
	Pro Met Gly Gly Pro Leu Pro Arg Ile Pro Gln Asn Val Met Ala Ile	
	340 345 350	
50	ggg ggg aat tca ggg ata gtt cat cca tca aca ggg tac atg gtg gct	1104
	Gly Gly Asn Ser Gly Ile Val His Pro Ser Thr Gly Tyr Met Val Ala	
	355 360 365	
55	agg agc atg gct tta gca cca gta cta gct gaa gcc atc gtc gag ggg	1152

## 146

	Arg Ser Met Ala Leu Ala Pro Val Leu Ala Glu Ala Ile Val Glu Gly	
	370 375 380	
5	ctt ggc tca aca aga atg ata aga ggg tct caa ctt tac cat aga gtt Leu Gly Ser Thr Arg Met Ile Arg Gly Ser Gln Leu Tyr His Arg Val 385 390 395 400	1200
10	tgg aat ggt ttg tgg cct ttg gat aga aga tgt gtt aga gaa tgt tat Trp Asn Gly Leu Trp Pro Leu Asp Arg Arg Cys Val Arg Glu Cys Tyr 405 410 415	1248
15	tca ttt ggg atg gag aca ttg ttg aag ctt gat ttg aaa ggg act agg Ser Phe Gly Met Glu Thr Leu Leu Lys Leu Asp Leu Lys Gly Thr Arg 420 425 430	1296
20	aga ttg ttt gac gct ttc ttt gat ctt gat cct aaa tac tgg caa ggg Arg Leu Phe Asp Ala Phe Phe Asp Leu Asp Pro Lys Tyr Trp Gln Gly 435 440 445	1344
25	ttc ctt tct tca aga ttg tct gtc aaa gaa ctt ggt tta ctc agc ttg Phe Leu Ser Ser Arg Leu Ser Val Lys Glu Leu Gly Leu Leu Ser Leu 450 455 460	1392
30	tgt ctt ttc gga cat ggc tca aac atg act agg ttg gat att gtt aca Cys Leu Phe Gly His Gly Ser Asn Met Thr Arg Leu Asp Ile Val Thr 465 470 475 480	1440
35	aaa tgt cct ctt cct ttg gtt aga ctg att ggc aat cta gca ata gag Lys Cys Pro Leu Pro Leu Val Arg Leu Ile Gly Asn Leu Ala Ile Glu 485 490 495	1488
40	agc ctt tgaatgtgaa aagtttgaat cattttcttc attttaattt ctttgattat Ser Leu	1544
	tttcatattt tctcaattgc aaaagtgaga taagagctac atactgtcaa caaataaact actattggaa agttaaaata tgtgtttggt gtatgttatt ctaatggaat ggattttgta aa	1604 1664 1666

&lt;211&gt; 498

&lt;212&gt; PRT

5 &lt;213&gt; Lycopersicon esculentum

&lt;400&gt; 108

10

Met Glu Ala Leu Leu Lys Pro Phe Pro Ser Leu Leu Leu Ser Ser Pro  
 1 5 10 15

15 Thr Pro His Arg Ser Ile Phe Gln Gln Asn Pro Ser Phe Leu Ser Pro  
 20 25 30

20 Thr Thr Lys Lys Lys Ser Arg Lys Cys Leu Leu Arg Asn Lys Ser Ser  
 35 40 45

Lys Leu Phe Cys Ser Phe Leu Asp Leu Ala Pro Thr Ser Lys Pro Glu  
 50 55 60

25

Ser Leu Asp Val Asn Ile Ser Trp Val Asp Pro Asn Ser Asn Arg Ala  
 65 70 75 80

30

Gln Phe Asp Val Ile Ile Ile Gly Ala Gly Pro Ala Gly Leu Arg Leu  
 85 90 95

35 Ala Glu Gln Val Ser Lys Tyr Gly Ile Lys Val Cys Cys Val Asp Pro  
 100 105 110

40 Ser Pro Leu Ser Met Trp Pro Asn Asn Tyr Gly Val Trp Val Asp Glu  
 115 120 125

Phe Glu Asn Leu Gly Leu Glu Asn Cys Leu Asp His Lys Trp Pro Met  
 130 135 140

45

Thr Cys Val His Ile Asn Asp Asn Lys Thr Lys Tyr Leu Gly Arg Pro  
 145 150 155 160

5

Tyr Gly Arg Val Ser Arg Lys Lys Leu Lys Leu Lys Leu Leu Asn Ser  
 165 170 175

10

Cys Val Glu Asn Arg Val Lys Phe Tyr Lys Ala Lys Val Trp Lys Val  
 180 185 190

15

Glu His Glu Glu Phe Glu Ser Ser Ile Val Cys Asp Asp Gly Lys Lys  
 195 200 205

20

Ile Arg Gly Ser Leu Val Val Asp Ala Ser Gly Phe Ala Ser Asp Phe  
 210 215 220

25

Ile Glu Tyr Asp Arg Pro Arg Asn His Gly Tyr Gln Ile Ala His Gly  
 225 230 235 240

30

Val Leu Val Glu Val Asp Asn His Pro Phe Asp Leu Asp Lys Met Val  
 245 250 255

35

Leu Met Asp Trp Arg Asp Ser His Leu Gly Asn Glu Pro Tyr Leu Arg  
 260 265 270

40

Val Asn Asn Ala Lys Glu Pro Thr Phe Leu Tyr Ala Met Pro Phe Asp  
 275 280 285

45

Arg Asp Leu Val Phe Leu Glu Glu Thr Ser Leu Val Ser Arg Pro Val  
 290 295 300

Leu Ser Tyr Met Glu Val Lys Arg Arg Met Val Ala Arg Leu Arg His  
 305 310 315 320



149

Leu Gly Ile Lys Val Lys Ser Val Ile Glu Glu Glu Lys Cys Val Ile  
 325 330 335

5 Pro Met Gly Gly Pro Leu Pro Arg Ile Pro Gln Asn Val Met Ala Ile  
 340 345 350

10 Gly Gly Asn Ser Gly Ile Val His Pro Ser Thr Gly Tyr Met Val Ala  
 355 360 365

15 Arg Ser Met Ala Leu Ala Pro Val Leu Ala Glu Ala Ile Val Glu Gly  
 370 375 380

Leu Gly Ser Thr Arg Met Ile Arg Gly Ser Gln Leu Tyr His Arg Val  
 385 390 395 400

20 Trp Asn Gly Leu Trp Pro Leu Asp Arg Arg Cys Val Arg Glu Cys Tyr  
 405 410 415

25 Ser Phe Gly Met Glu Thr Leu Leu Lys Leu Asp Leu Lys Gly Thr Arg  
 420 425 430

30 Arg Leu Phe Asp Ala Phe Phe Asp Leu Asp Pro Lys Tyr Trp Gln Gly  
 435 440 445

35 Phe Leu Ser Ser Arg Leu Ser Val Lys Glu Leu Gly Leu Leu Ser Leu  
 450 455 460

Cys Leu Phe Gly His Gly Ser Asn Met Thr Arg Leu Asp Ile Val Thr  
 465 470 475 480

40 Lys Cys Pro Leu Pro Leu Val Arg Leu Ile Gly Asn Leu Ala Ile Glu  
 485 490 495

45 Ser Leu

5 <210> 109  
 <211> 1125  
 <212> DNA  
 10 <213> Lycopersicon esculentum  
 15 <220>  
 <221> CDS  
 <222> (20)..(946)  
 20 <223>  
 <400> 109  
 25 ttggtcatct ccacaatca atg gct gcc gcc gcc aga atc tcc gcc tcc tct 52  
 Met Ala Ala Ala Ala Arg Ile Ser Ala Ser Ser  
 1 5 10  
 acc tca cga act ttt tat ttc cgt cat tca ccg ttt ctt ggc cca aaa 100  
 30 Thr Ser Arg Thr Phe Tyr Phe Arg His Ser Pro Phe Leu Gly Pro Lys  
 15 20 25  
 cct act ttcg aca acc tca cat gtt tct cca atc tct cct ttt tct ctt 148  
 Pro Thr Ser Thr Thr Ser His Val Ser Pro Ile Ser Pro Phe Ser Leu  
 35 30 35 40  
 aat cta ggc cca att ttg agg tct aga aga aaa ccc agt ttc act gtt 196  
 Asn Leu Gly Pro Ile Leu Arg Ser Arg Arg Lys Pro Ser Phe Thr Val  
 45 50 55  
 40 tgc ttt gtt ctc gag gat gag aag ctg aaa cct caa ttt gac gat gag 244  
 Cys Phe Val Leu Glu Asp Glu Lys Leu Lys Pro Gln Phe Asp Asp Glu  
 60 65 70 75  
 45 gct gag gat ttt gaa aag aag att gag gaa cag atc tta gct act cgc 292

151

	Ala	Glu	Asp	Phe	Glu	Lys	Lys	Ile	Glu	Glu	Gln	Ile	Leu	Ala	Thr	Arg	
					80				85						90		
	ttg	gcg	gag	aaa	ctg	gct	agg	aag	aaa	tcg	gag	agg	ttt	act	tat	ctt	340
5	Leu	Ala	Glu	Lys	Leu	Ala	Arg	Lys	Lys	Ser	Glu	Arg	Phe	Thr	Tyr	Leu	
				95					100				105				
	gtg	gct	gct	ata	atg	tct	agt	ttt	ggg	att	act	tct	atg	gct	gtt	atg	388
10	Val	Ala	Ala	Ile	Met	Ser	Ser	Phe	Gly	Ile	Thr	Ser	Met	Ala	Val	Met	
				110					115				120				
	gct	gtt	tat	tac	aga	ttt	tcg	tgg	caa	atg	gag	gga	gga	gaa	gtt	cct	436
	Ala	Val	Tyr	Tyr	Arg	Phe	Ser	Trp	Gln	Met	Glu	Gly	Gly	Glu	Val	Pro	
				125				130				135					
15	gta	acc	gaa	atg	ttg	ggt	aca	ttt	gct	ctc	tct	gtt	ggt	gct	gct	gta	484
	Val	Thr	Glu	Met	Leu	Gly	Thr	Phe	Ala	Leu	Ser	Val	Gly	Ala	Ala	Val	
				140			145				150				155		
	gga	atg	gag	ttt	tgg	gcg	aga	tgg	gca	cac	aaa	gca	ctg	tgg	cat	gct	532
20	Gly	Met	Glu	Phe	Trp	Ala	Arg	Trp	Ala	His	Lys	Ala	Leu	Trp	His	Ala	
					160					165					170		
	tca	cta	tgg	cac	atg	cat	gag	tca	cac	cac	aaa	cca	aga	gaa	gga	cct	580
25	Ser	Leu	Trp	His	Met	His	Glu	Ser	His	His	Lys	Pro	Arg	Glu	Gly	Pro	
				175					180					185			
	ttt	gag	ctg	aac	gac	gtt	ttc	gcc	ata	aca	aac	gct	gtt	cca	gca	ata	628
	Phe	Glu	Leu	Asn	Asp	Val	Phe	Ala	Ile	Thr	Asn	Ala	Val	Pro	Ala	Ile	
30				190				195					200				
	gcc	ctc	ctc	aac	tat	ggt	ttc	ttc	cat	aaa	ggc	ctc	att	gcc	gga	cta	676
	Ala	Leu	Leu	Asn	Tyr	Gly	Phe	Phe	His	Lys	Gly	Leu	Ile	Ala	Gly	Leu	
				205			210				215						
35	tgc	ttc	ggt	gct	ggg	cta	ggg	atc	aca	gta	ttt	gga	atg	gca	tac	atg	724
	Cys	Phe	Gly	Ala	Gly	Leu	Gly	Ile	Thr	Val	Phe	Gly	Met	Ala	Tyr	Met	
				220			225				230				235		
	ttt	gtt	cac	gat	ggt	ttg	gtt	cac	aag	aga	ttc	cca	gtt	gga	cct	gta	772
40	Phe	Val	His	Asp	Gly	Leu	Val	His	Lys	Arg	Phe	Pro	Val	Gly	Pro	Val	
					240				245					250			
	gcc	aat	gta	cct	tat	ctt	agg	aag	gtg	gct	gct	gct	cat	tcg	ctt	cat	820
45	Ala	Asn	Val	Pro	Tyr	Leu	Arg	Lys	Val	Ala	Ala	Ala	His	Ser	Leu	His	

255 260 265  
 cac tca gag aag ttc aat ggt gtc cca tat ggc ttg ttc ttc gga cct 868  
 His Ser Glu Lys Phe Asn Gly Val Pro Tyr Gly Leu Phe Phe Gly Pro  
 5 270 275 280  
 aag gaa ctg gaa gaa gta gga ggg acg gaa gag ttg gaa aag gaa gtg 916  
 Lys Glu Leu Glu Glu Val Gly Gly Thr Glu Glu Leu Glu Lys Glu Val  
 285 290 295  
 10 ata cga agg acg aga ctt tcg aaa gga tca tgaacgattg ttcataaaca 966  
 Ile Arg Arg Thr Arg Leu Ser Lys Gly Ser  
 300 305  
 15 tagaatgtca ttttacactt cttatcaatg aggaaggggtg atttttgatg tatttgatag 1026  
 tagagaaaaa tgtagctctc ttgatgaaat gaatttgat ttatgtaggc tcttcttatt 1086  
 cagtaagatt ttttcttttt ttgatctcg tgccgaatt 1125  
 20  
 <210> 110  
 <211> 309  
 25 <212> PRT  
 <213> Lycopersicon esculentum  
 30  
 <400> 110  
 Met Ala Ala Ala Ala Arg Ile Ser Ala Ser Ser Thr Ser Arg Thr Phe  
 35 1 5 10 15  
 Tyr Phe Arg His Ser Pro Phe Leu Gly Pro Lys Pro Thr Ser Thr Thr  
 20 25 30  
 40 Ser His Val Ser Pro Ile Ser Pro Phe Ser Leu Asn Leu Gly Pro Ile  
 35 40 45  
 45

## 153

Leu Arg Ser Arg Arg Lys Pro Ser Phe Thr Val Cys Phe Val Leu Glu  
 50 55 60

5 Asp Glu Lys Leu Lys Pro Gln Phe Asp Asp Glu Ala Glu Asp Phe Glu  
 65 70 75 80

10 Lys Lys Ile Glu Glu Gln Ile Leu Ala Thr Arg Leu Ala Glu Lys Leu  
 85 90 95

15 Ala Arg Lys Lys Ser Glu Arg Phe Thr Tyr Leu Val Ala Ala Ile Met  
 100 105 110

Ser Ser Phe Gly Ile Thr Ser Met Ala Val Met Ala Val Tyr Tyr Arg  
 115 120 125

20 Phe Ser Trp Gln Met Glu Gly Gly Glu Val Pro Val Thr Glu Met Leu  
 130 135 140

25 Gly Thr Phe Ala Leu Ser Val Gly Ala Ala Val Gly Met Glu Phe Trp  
 145 150 155 160

30 Ala Arg Trp Ala His Lys Ala Leu Trp His Ala Ser Leu Trp His Met  
 165 170 175

35 His Glu Ser His His Lys Pro Arg Glu Gly Pro Phe Glu Leu Asn Asp  
 180 185 190

Val Phe Ala Ile Thr Asn Ala Val Pro Ala Ile Ala Leu Leu Asn Tyr  
 195 200 205

40 Gly Phe Phe His Lys Gly Leu Ile Ala Gly Leu Cys Phe Gly Ala Gly  
 210 215 220

45 Leu Gly Ile Thr Val Phe Gly Met Ala Tyr Met Phe Val His Asp Gly

154

225

230

235

240

5

Leu Val His Lys Arg Phe Pro Val Gly Pro Val Ala Asn Val Pro Tyr  
 245 250 255

10

Leu Arg Lys Val Ala Ala Ala His Ser Leu His His Ser Glu Lys Phe  
 260 265 270

15

Asn Gly Val Pro Tyr Gly Leu Phe Phe Gly Pro Lys Glu Leu Glu Glu  
 275 280 285

Val Gly Gly Thr Glu Glu Leu Glu Lys Glu Val Ile Arg Arg Thr Arg  
 290 295 300

20

Leu Ser Lys Gly Ser  
 305

25

&lt;210&gt; 111

&lt;211&gt; 1779

&lt;212&gt; DNA

30

&lt;213&gt; Arabidopsis thaliana

35

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1)..(1779)

40

&lt;223&gt;

&lt;400&gt; 111

45

atg gat ctc cgt cgg agg cct cct aaa cca ccg gtt acc aac aac aac

48

## 155

	Met	Asp	Leu	Arg	Arg	Arg	Pro	Pro	Lys	Pro	Pro	Val	Thr	Asn	Asn	Asn	
	1				5					10					15		
	aac tcc aac gga tct ttc cgt tct tat cag cct cgc act tcc gat gac																96
5	Asn	Ser	Asn	Gly	Ser	Phe	Arg	Ser	Tyr	Gln	Pro	Arg	Thr	Ser	Asp	Asp	
			20						25					30			
	gat cat cgt cgc cgg gct aca aca att gct cct cca ccg aaa gca tcc																144
10	Asp	His	Arg	Arg	Arg	Ala	Thr	Thr	Ile	Ala	Pro	Pro	Pro	Lys	Ala	Ser	
			35					40					45				
	gac gcg ctt cct ctt ccg tta tat ctc aca aac gcc gtt ttc ttc acg																192
	Asp	Ala	Leu	Pro	Leu	Pro	Leu	Tyr	Leu	Thr	Asn	Ala	Val	Phe	Phe	Thr	
15			50				55					60					
	ctc ttc ttc tcc gtc gcg tat tac ctc ctc cac cgg tgg cgt gac aag																240
	Leu	Phe	Phe	Ser	Val	Ala	Tyr	Tyr	Leu	Leu	His	Arg	Trp	Arg	Asp	Lys	
			65			70				75					80		
20	atc cgt tac aat acg cct ctt cac gtc gtc act atc aca gaa ctc ggc																288
	Ile	Arg	Tyr	Asn	Thr	Pro	Leu	His	Val	Val	Thr	Ile	Thr	Glu	Leu	Gly	
				85					90					95			
	gcc att att gct ctc atc gct tcg ttt atc tat ctc cta ggg ttt ttt																336
25	Ala	Ile	Ile	Ala	Leu	Ile	Ala	Ser	Phe	Ile	Tyr	Leu	Leu	Gly	Phe	Phe	
				100					105					110			
	ggc att gac ttt gtt cag tca ttt atc tca cgt gcc tct ggt gat gct																384
30	Gly	Ile	Asp	Phe	Val	Gln	Ser	Phe	Ile	Ser	Arg	Ala	Ser	Gly	Asp	Ala	
			115				120					125					
	tgg gat ctc gcc gat acg atc gat gat gat gac cac cgc ctt gtc acg																432
	Trp	Asp	Leu	Ala	Asp	Thr	Ile	Asp	Asp	Asp	Asp	His	Arg	Leu	Val	Thr	
35			130				135					140					
	tgc tct cca ccg act ccg atc gtt tcc gtt gct aaa tta cct aat ccg																480
	Cys	Ser	Pro	Pro	Thr	Pro	Ile	Val	Ser	Val	Ala	Lys	Leu	Pro	Asn	Pro	
			145			150				155				160			
40	gaa cct att gtt acc gaa tcg ctt cct gag gaa gac gag gag att gtg																528
	Glu	Pro	Ile	Val	Thr	Glu	Ser	Leu	Pro	Glu	Glu	Asp	Glu	Glu	Ile	Val	
				165					170					175			
	aaa tcg gtt atc gac gga gtt att cca tcg tac tcg ctt gaa tct cgt																576
45	Lys	Ser	Val	Ile	Asp	Gly	Val	Ile	Pro	Ser	Tyr	Ser	Leu	Glu	Ser	Arg	

	180	185	190	
	ctc ggt gat tgc aaa aga gcg gcg tcg att cgt cgt gag gcg ttg cag			624
	Leu Gly Asp Cys Lys Arg Ala Ala Ser Ile Arg Arg Glu Ala Leu Gln			
5	195	200	205	
	aga gtc acc ggg aga tcg att gaa ggg tta ccg ttg gat gga ttt gat			672
	Arg Val Thr Gly Arg Ser Ile Glu Gly Leu Pro Leu Asp Gly Phe Asp			
	210	215	220	
10				
	tat gaa tcg att ttg ggg caa tgc tgt gag atg cct gtt gga tac att			720
	Tyr Glu Ser Ile Leu Gly Gln Cys Cys Glu Met Pro Val Gly Tyr Ile			
	225	230	235	240
15	cag att cct gtt ggg att gct ggt cca ttg ttg ctt gat ggt tat gag			768
	Gln Ile Pro Val Gly Ile Ala Gly Pro Leu Leu Leu Asp Gly Tyr Glu			
	245	250	255	
	tac tct gtt cct atg gct aca acc gaa ggt tgt ttg gtt gct agc act			816
20	Tyr Ser Val Pro Met Ala Thr Thr Glu Gly Cys Leu Val Ala Ser Thr			
	260	265	270	
	aac aga ggc tgc aag gct atg ttt atc tct ggt ggc gcc acc agt acc			864
	Asn Arg Gly Cys Lys Ala Met Phe Ile Ser Gly Gly Ala Thr Ser Thr			
25	275	280	285	
	gtt ctt aag gac ggt atg acc cga gca cct gtt gtt cgg ttc gct tcg			912
	Val Leu Lys Asp Gly Met Thr Arg Ala Pro Val Val Arg Phe Ala Ser			
	290	295	300	
30				
	gcg aga cga gct tcg gag ctt aag ttt ttc ttg gag aat cca gag aac			960
	Ala Arg Arg Ala Ser Glu Leu Lys Phe Phe Leu Glu Asn Pro Glu Asn			
	305	310	315	320
35	ttt gat act ttg gca gta gtc ttc aac agg tcg agt aga ttt gca aga			1008
	Phe Asp Thr Leu Ala Val Val Phe Asn Arg Ser Ser Arg Phe Ala Arg			
	325	330	335	
	ctg caa agt gtt aaa tgc aca atc gcg ggg aag aat gct tat gta agg			1056
40	Leu Gln Ser Val Lys Cys Thr Ile Ala Gly Lys Asn Ala Tyr Val Arg			
	340	345	350	
	ttc tgt tgt agt act ggt gat gct atg ggg atg aat atg gtt tct aaa			1104
	Phe Cys Cys Ser Thr Gly Asp Ala Met Gly Met Asn Met Val Ser Lys			
45	355	360	365	



	ggt gtg cag aat gtt ctt gag tat ctt acc gat gat ttc cct gac atg Gly Val Gln Asn Val Leu Glu Tyr Leu Thr Asp Asp Phe Pro Asp Met 370 375 380	1152
5	gat gtg att gga atc tct ggt aac ttc tgt tcg gac aag aaa cct gct Asp Val Ile Gly Ile Ser Gly Asn Phe Cys Ser Asp Lys Lys Pro Ala 385 390 395 400	1200
10	gct gtg aac tgg att gag gga cgt ggt aaa tca gtt gtt tgc gag gct Ala Val Asn Trp Ile Glu Gly Arg Gly Lys Ser Val Val Cys Glu Ala 405 410 415	1248
15	gta atc aga gga gag atc gtg aac aag gtc ttg aaa acg agc gtg gct Val Ile Arg Gly Glu Ile Val Asn Lys Val Leu Lys Thr Ser Val Ala 420 425 430	1296
20	gct tta gtc gag ctc aac atg ctc aag aac cta gct ggc tct gct gtt Ala Leu Val Glu Leu Asn Met Leu Lys Asn Leu Ala Gly Ser Ala Val 435 440 445	1344
25	gca ggc tct cta ggt gga ttc aac gct cat gcc agt aac ata gtg tct Ala Gly Ser Leu Gly Gly Phe Asn Ala His Ala Ser Asn Ile Val Ser 450 455 460	1392
30	gct gta ttc ata gct act ggc caa gat cca gct caa aac gtg gag agt Ala Val Phe Ile Ala Thr Gly Gln Asp Pro Ala Gln Asn Val Glu Ser 465 470 475 480	1440
35	tct caa tgc atc acc atg atg gaa gct att aat gac ggc aaa gat atc Ser Gln Cys Ile Thr Met Met Glu Ala Ile Asn Asp Gly Lys Asp Ile 485 490 495	1488
40	cat atc tca gtc act atg cca tct atc gag gtg ggg aca gtg gga gga His Ile Ser Val Thr Met Pro Ser Ile Glu Val Gly Thr Val Gly Gly 500 505 510	1536
45	gga aca cag ctt gca tct caa tca gcg tgt tta aac ctg ctc gga gtt Gly Thr Gln Leu Ala Ser Gln Ser Ala Cys Leu Asn Leu Leu Gly Val 515 520 525	1584
	aaa gga gca agc aca gag tcg ccg gga atg aac gca agg agg cta gcg Lys Gly Ala Ser Thr Glu Ser Pro Gly Met Asn Ala Arg Arg Leu Ala 530 535 540	1632

158

acg atc gta gcc gga gca gtt tta gct gga gag tta tct tta atg tca 1680  
 Thr Ile Val Ala Gly Ala Val Leu Ala Gly Glu Leu Ser Leu Met Ser  
 545 550 555 560

5 gca att gca gct gga cag ctt gtg aga agt cac atg aaa tac aat aga 1728  
 Ala Ile Ala Ala Gly Gln Leu Val Arg Ser His Met Lys Tyr Asn Arg  
 565 570 575

10 tcc agc cga gac atc tct gga gca acg aca acg aca aca aca aca aca 1776  
 Ser Ser Arg Asp Ile Ser Gly Ala Thr Thr Thr Thr Thr Thr Thr Thr  
 580 585 590

tga 1779

15 <210> 112  
 <211> 592

20 <212> PRT  
 <213> Arabidopsis thaliana

25 <400> 112

Met Asp Leu Arg Arg Arg Pro Pro Lys Pro Pro Val Thr Asn Asn Asn  
 1 5 10 15

30 Asn Ser Asn Gly Ser Phe Arg Ser Tyr Gln Pro Arg Thr Ser Asp Asp  
 20 25 30

35 Asp His Arg Arg Arg Ala Thr Thr Ile Ala Pro Pro Pro Lys Ala Ser  
 35 40 45

40 Asp Ala Leu Pro Leu Pro Leu Tyr Leu Thr Asn Ala Val Phe Phe Thr  
 50 55 60

45 Leu Phe Phe Ser Val Ala Tyr Tyr Leu Leu His Arg Trp Arg Asp Lys  
 65 70 75 80

	Ile	Arg	Tyr	Asn	Thr	Pro	Leu	His	Val	Val	Thr	Ile	Thr	Glu	Leu	Gly	
					85					90						95	
5																	
	Ala	Ile	Ile	Ala	Leu	Ile	Ala	Ser	Phe	Ile	Tyr	Leu	Leu	Gly	Phe	Phe	
				100					105					110			
10																	
	Gly	Ile	Asp	Phe	Val	Gln	Ser	Phe	Ile	Ser	Arg	Ala	Ser	Gly	Asp	Ala	
			115					120						125			
15																	
	Trp	Asp	Leu	Ala	Asp	Thr	Ile	Asp	Asp	Asp	Asp	His	Arg	Leu	Val	Thr	
		130					135					140					
20																	
	Cys	Ser	Pro	Pro	Thr	Pro	Ile	Val	Ser	Val	Ala	Lys	Leu	Pro	Asn	Pro	
	145					150					155					160	
25																	
	Glu	Pro	Ile	Val	Thr	Glu	Ser	Leu	Pro	Glu	Glu	Asp	Glu	Glu	Ile	Val	
					165					170					175		
30																	
	Lys	Ser	Val	Ile	Asp	Gly	Val	Ile	Pro	Ser	Tyr	Ser	Leu	Glu	Ser	Arg	
			180						185					190			
35																	
	Leu	Gly	Asp	Cys	Lys	Arg	Ala	Ala	Ser	Ile	Arg	Arg	Glu	Ala	Leu	Gln	
			195					200					205				
40																	
	Arg	Val	Thr	Gly	Arg	Ser	Ile	Glu	Gly	Leu	Pro	Leu	Asp	Gly	Phe	Asp	
		210					215					220					
45																	
	Tyr	Glu	Ser	Ile	Leu	Gly	Gln	Cys	Cys	Glu	Met	Pro	Val	Gly	Tyr	Ile	
	225				230					235						240	
50																	
	Gln	Ile	Pro	Val	Gly	Ile	Ala	Gly	Pro	Leu	Leu	Leu	Asp	Gly	Tyr	Glu	
					245				250						255		

160

Tyr Ser Val Pro Met Ala Thr Thr Glu Gly Cys Leu Val Ala Ser Thr  
 260 265 270

5

Asn Arg Gly Cys Lys Ala Met Phe Ile Ser Gly Gly Ala Thr Ser Thr  
 275 280 285

10

Val Leu Lys Asp Gly Met Thr Arg Ala Pro Val Val Arg Phe Ala Ser  
 290 295 300

15

Ala Arg Arg Ala Ser Glu Leu Lys Phe Phe Leu Glu Asn Pro Glu Asn  
 305 310 315 320

20

Phe Asp Thr Leu Ala Val Val Phe Asn Arg Ser Ser Arg Phe Ala Arg  
 325 330 335

Leu Gln Ser Val Lys Cys Thr Ile Ala Gly Lys Asn Ala Tyr Val Arg  
 340 345 350

25

Phe Cys Cys Ser Thr Gly Asp Ala Met Gly Met Asn Met Val Ser Lys  
 355 360 365

30

Gly Val Gln Asn Val Leu Glu Tyr Leu Thr Asp Asp Phe Pro Asp Met  
 370 375 380

35

Asp Val Ile Gly Ile Ser Gly Asn Phe Cys Ser Asp Lys Lys Pro Ala  
 385 390 395 400

40

Ala Val Asn Trp Ile Glu Gly Arg Gly Lys Ser Val Val Cys Glu Ala  
 405 410 415

Val Ile Arg Gly Glu Ile Val Asn Lys Val Leu Lys Thr Ser Val Ala  
 420 425 430

45

## 161

Ala Leu Val Glu Leu Asn Met Leu Lys Asn Leu Ala Gly Ser Ala Val  
 435 440 445

5 Ala Gly Ser Leu Gly Gly Phe Asn Ala His Ala Ser Asn Ile Val Ser  
 450 455 460

10 Ala Val Phe Ile Ala Thr Gly Gln Asp Pro Ala Gln Asn Val Glu Ser  
 465 470 475 480

Ser Gln Cys Ile Thr Met Met Glu Ala Ile Asn Asp Gly Lys Asp Ile  
 485 490 495

15 His Ile Ser Val Thr Met Pro Ser Ile Glu Val Gly Thr Val Gly Gly  
 500 505 510

20 Gly Thr Gln Leu Ala Ser Gln Ser Ala Cys Leu Asn Leu Leu Gly Val  
 515 520 525

25 Lys Gly Ala Ser Thr Glu Ser Pro Gly Met Asn Ala Arg Arg Leu Ala  
 530 535 540

30 Thr Ile Val Ala Gly Ala Val Leu Ala Gly Glu Leu Ser Leu Met Ser  
 545 550 555 560

Ala Ile Ala Ala Gly Gln Leu Val Arg Ser His Met Lys Tyr Asn Arg  
 565 570 575

35 Ser Ser Arg Asp Ile Ser Gly Ala Thr Thr Thr Thr Thr Thr Thr Thr  
 580 585 590

40 <210> 113  
 <211> 1401

&lt;212&gt; DNA

&lt;213&gt; Arabidopsis thaliana ISPH

5

&lt;220&gt;

&lt;221&gt; CDS

10

&lt;222&gt; (1)..(1401)

&lt;223&gt;

15

&lt;400&gt; 113

atg gct gtt gcg ctc, caa ttc agc cga tta tgc gtt cga ccg gat act 48  
 Met Ala Val Ala Leu Gln Phe Ser Arg Leu Cys Val Arg Pro Asp Thr

20

1 5 10 15

ttc gtg cgg gag aat cat ctc tct gga tcc gga tct ctc cgc cgc cgg 96  
 Phe Val Arg Glu Asn His Leu Ser Gly Ser Gly Ser Leu Arg Arg Arg

25

20 25 30

aaa gct tta tca gtc cgg tgc tcg tct ggc gat gag aac gct cct tcg 144  
 Lys Ala Leu Ser Val Arg Cys Ser Ser Gly Asp Glu Asn Ala Pro Ser

30

35 40 45

cca tcg gtg gtg atg gac tcc gat ttc gac gcc aag gtg ttc cgt aag 192  
 Pro Ser Val Val Met Asp Ser Asp Phe Asp Ala Lys Val Phe Arg Lys

35

50 55 60

aac ttg acg aga agc gat aat tac aat cgt aaa ggg ttc ggt cat aag 240  
 Asn Leu Thr Arg Ser Asp Asn Tyr Asn Arg Lys Gly Phe Gly His Lys

40

65 70 75 80

gag gag aca ctc aag ctc atg aat cga gag tac acc agt gat ata ttg 288  
 Glu Glu Thr Leu Lys Leu Met Asn Arg Glu Tyr Thr Ser Asp Ile Leu

45

85 90 95

gag aca ctg aaa aca aat ggg tat act tat tct tgg gga gat gtt act 336  
 Glu Thr Leu Lys Thr Asn Gly Tyr Thr Tyr Ser Trp Gly Asp Val Thr

45

100 105 110

## 163

	gtg aaa ctc gct aaa gca tat ggt ttt tgc tgg ggt gtt gag cgt gct Val Lys Leu Ala Lys Ala Tyr Gly Phe Cys Trp Gly Val Glu Arg Ala 115 120 125	384
5	ggt cag att gca tat gaa gca cga aag cag ttt cca gag gag agg ctt Val Gln Ile Ala Tyr Glu Ala Arg Lys Gln Phe Pro Glu Glu Arg Leu 130 135 140	432
10	tgg att act aac gaa atc att cat aac ccg acc gtc aat aag agg ttg Trp Ile Thr Asn Glu Ile Ile His Asn Pro Thr Val Asn Lys Arg Leu 145 150 155 160	480
15	gaa gat atg gat gtt aaa att att ccg gtt gag gat tca aag aaa cag Glu Asp Met Asp Val Lys Ile Ile Pro Val Glu Asp Ser Lys Lys Gln 165 170 175	528
20	ttt gat gta gta gag aaa gat gat gtg gtt atc ctt cct gcg ttt gga Phe Asp Val Val Glu Lys Asp Asp Val Val Ile Leu Pro Ala Phe Gly 180 185 190	576
	gct ggt gtt gac gag atg tat gtt ctt aat gat aaa aag gtg caa att Ala Gly Val Asp Glu Met Tyr Val Leu Asn Asp Lys Lys Val Gln Ile 195 200 205	624
25	ggt gac acg act tgt cct tgg gtg aca aag gtc tgg aac acg gtt gag Val Asp Thr Thr Cys Pro Trp Val Thr Lys Val Trp Asn Thr Val Glu 210 215 220	672
30	aag cac aag aag ggg gaa tac aca tca gta atc cat ggt aaa tat aat Lys His Lys Lys Gly Glu Tyr Thr Ser Val Ile His Gly Lys Tyr Asn 225 " 230 235 240	720
35	cat gaa gag acg att gca act gcg tct ttt gca gga aag tac atc att His Glu Glu Thr Ile Ala Thr Ala Ser Phe Ala Gly Lys Tyr Ile Ile 245 250 255	768
40	gta aag aac atg aaa gag gca aat tac gtt tgt gat tac att ctc ggt Val Lys Asn Met Lys Glu Ala Asn Tyr Val Cys Asp Tyr Ile Leu Gly 260 265 270	816
	ggc caa tac gat gga tct agc tcc aca aaa gag gag ttc atg gag aaa Gly Gln Tyr Asp Gly Ser Ser Ser Thr Lys Glu Glu Phe Met Glu Lys 275 280 285	864
45	ttc aaa tac gca att tcg aag ggt ttc gat ccc gac aat gac ctt gtc	912

164

Phe Lys Tyr Ala Ile Ser Lys Gly Phe Asp Pro Asp Asn Asp Leu Val  
290 295 300

aaa gtt ggt att gca aac caa aca acg atg cta aag gga gaa aca gag  
5 Lys Val Gly Ile Ala Asn Gln Thr Thr Met Leu Lys Gly Glu Thr Glu  
305                    310                    315                    320

gag ata gga aga tta ctc gag aca aca atg atg cgc aag tat gga gtg 1008  
Glu Ile Gly Arg Leu Leu Glu Thr Thr Met Met Arg Lys Tyr Gly Val  
10 325 330 335

gaa aat gta agc gga cat ttc atc agc ttc aac aca ata tgc gac gct . 1056  
Glu Asn Val Ser Gly His Phe Ile Ser Phe Asn Thr Ile Cys Asp Ala  
340 345 350

act caa gag cga caa gac gca atc tat gag cta gtg gaa gag aag att 1104  
Thr Gln Glu Arg Gln Asp Ala Ile Tyr Glu Leu Val Glu Glu Lys Ile  
355 360 365

20 gac ctc atg cta gtg gtt ggc gga tgg aat tca agt aac acc tct cac . 1152  
Asp Leu Met Leu Val Val Gly Gly Trp Asn Ser Ser Asn Thr Ser His  
370 375 380

25    ctt cag gaa atc tca gag gca cgg gga atc cca tct tac tgg atc gat    1200  
       Leu Gln Glu Ile Ser Glu Ala Arg Gly Ile Pro Ser Tyr Trp Ile Asp  
       385                    390                    395                    400

30 agt gag aaa cgg ata gga cct ggg aat aaa ata gcc tat aag ctc cac 1248  
Ser Glu Lys Arg Ile Gly Pro Gly Asn Lys Ile Ala Tyr Lys Leu His  
405 410 415

tat gga gaa ctg gtc gag aag gaa aac ttt ctc cca aag gga cca ata 1296  
Tyr Gly Glu Leu Val Glu Lys Glu Asn Phe Leu Pro Lys Gly Pro Ile  
420 425 430

aca atc ggt gtg aca tca ggt gca tca acc ccg gat aag gtc gtg gaa 1344  
Thr Ile Gly Val Thr Ser Gly Ala Ser Thr Pro Asp Lys Val Val Glu  
435 440 445

40    gat gct ttg gtg aag gtg ttc gac att aaa cgt gaa gag tta ttg cag                      1392  
       Asp Ala Leu Val Lys Val Phe Asp Ile Lys Arg Glu Glu Leu Leu Gln  
               450                      455                      460

ctg gct tga  
Leu Ala

1401



465

&lt;210&gt; 114

5

&lt;211&gt; 466

&lt;212&gt; PRT

10 &lt;213&gt; Arabidopsis thaliana ISPH

&lt;400&gt; 114

15

Met Ala Val Ala Leu Gln Phe Ser Arg Leu Cys Val Arg Pro Asp Thr  
1 5 10 15

Phe Val Arg Glu Asn His Leu Ser Gly Ser Gly Ser Leu Arg Arg Arg  
20 25 30

Lys Ala Leu Ser Val Arg Cys Ser Ser Gly Asp Glu Asn Ala Pro Ser  
25 35 40 45

Pro Ser Val Val Met Asp Ser Asp Phe Asp Ala Lys Val Phe Arg Lys  
50 55 60

30

Asn Leu Thr Arg Ser Asp Asn Tyr Asn Arg Lys Gly Phe Gly His Lys  
65 70 75 80

35

Glu Glu Thr Leu Lys Leu Met Asn Arg Glu Tyr Thr Ser Asp Ile Leu  
85 90 95

Glu Thr Leu Lys Thr Asn Gly Tyr Thr Tyr Ser Trp Gly Asp Val Thr  
100 105 110

Val Lys Leu Ala Lys Ala Tyr Gly Phe Cys Trp Gly Val Glu Arg Ala  
45 115 120 125

Val Gln Ile Ala Tyr Glu Ala Arg Lys Gln Phe Pro Glu Glu Arg Leu  
 130 135 140  
 5

Trp Ile Thr Asn Glu Ile Ile His Asn Pro Thr Val Asn Lys Arg Leu  
 145 150 155 160

10

Glu Asp Met Asp Val Lys Ile Ile Pro Val Glu Asp Ser Lys Lys Gln  
 165 170 175

15

Phe Asp Val Val Glu Lys Asp Asp Val Val Ile Leu Pro Ala Phe Gly  
 180 185 190

20

Ala Gly Val Asp Glu Met Tyr Val Leu Asn Asp Lys Lys Val Gln Ile  
 195 200 205

Val Asp Thr Thr Cys Pro Trp Val Thr Lys Val Trp Asn Thr Val Glu  
 210 215 220

25

Lys His Lys Lys Gly Glu Tyr Thr Ser Val Ile His Gly Lys Tyr Asn  
 225 230 235 240

30

His Glu Glu Thr Ile Ala Thr Ala Ser Phe Ala Gly Lys Tyr Ile Ile  
 245 250 255

35

Val Lys Asn Met Lys Glu Ala Asn Tyr Val Cys Asp Tyr Ile Leu Gly  
 260 265 270

40

Gly Gln Tyr Asp Gly Ser Ser Ser Thr Lys Glu Glu Phe Met Glu Lys  
 275 280 285

Phe Lys Tyr Ala Ile Ser Lys Gly Phe Asp Pro Asp Asn Asp Leu Val  
 290 295 300

45

Lys Val Gly Ile Ala Asn Gln Thr Thr Met Leu Lys Gly Glu Thr Glu  
 305 310 315 320

5

Glu Ile Gly Arg Leu Leu Glu Thr Thr Met Met Arg Lys Tyr Gly Val  
 325 330 335

10

Glu Asn Val Ser Gly His Phe Ile Ser Phe Asn Thr Ile Cys Asp Ala  
 340 345 350

15

Thr Gln Glu Arg Gln Asp Ala Ile Tyr Glu Leu Val Glu Glu Lys Ile  
 355 360 365

20

Asp Leu Met Leu Val Val Gly Gly Trp Asn Ser Ser Asn Thr Ser His  
 370 375 380

Leu Gln Glu Ile Ser Glu Ala Arg Gly Ile Pro Ser Tyr Trp Ile Asp  
 385 390 395 400

25

Ser Glu Lys Arg Ile Gly Pro Gly Asn Lys Ile Ala Tyr Lys Leu His  
 405 410 415

30

Tyr Gly Glu Leu Val Glu Lys Glu Asn Phe Leu Pro Lys Gly Pro Ile  
 420 425 430

35

Thr Ile Gly Val Thr Ser Gly Ala Ser Thr Pro Asp Lys Val Val Glu  
 435 440 445

40

Asp Ala Leu Val Lys Val Phe Asp Ile Lys Arg Glu Glu Leu Leu Gln  
 450 455 460

Leu Ala  
 465

45

&lt;210&gt; 115

&lt;211&gt; 2160

5 &lt;212&gt; DNA

&lt;213&gt; Lycopersicon esculentum

10

&lt;220&gt;

&lt;221&gt; CDS

15 &lt;222&gt; (1)..(2160)

&lt;223&gt;

20

&lt;400&gt; 115

atg gct ttg tgt gct tat gca ttt cct ggg att ttg aac agg act ggt 48

Met Ala Leu Cys Ala Tyr Ala Phe Pro Gly Ile Leu Asn Arg Thr Gly

1 5 10 15

25

gtg gtt tca gat tct tct aag gca acc cct ttg ttc tct gga tgg att 96

Val Val Ser Asp Ser Ser Lys Ala Thr Pro Leu Phe Ser Gly Trp Ile

20 25 30

30

cat gga aca gat ctg cag ttt ttg ttc caa cac aag ctt act cat gag 144

His Gly Thr Asp Leu Gln Phe Leu Phe Gln His Lys Leu Thr His Glu

35 40 45

gtc aag aaa agg tca cgt gtg gtt cag gct tcc tta tca gaa tct gga 192

35 Val Lys Lys Arg Ser Arg Val Val Gln Ala Ser Leu Ser Glu Ser Gly

50 55 60

gaa tac tac aca cag aga ccg cca acg cct att ttg gac act gtg aac 240

Glu Tyr Tyr Thr Gln Arg Pro Pro Thr Pro Ile Leu Asp Thr Val Asn

40 65 70 75 80

tat ccc att cat atg aaa aat ctg tct ctg aag gaa ctt aaa caa cta 288

Tyr Pro Ile His Met Lys Asn Leu Ser Leu Lys Glu Leu Lys Gln Leu

85 90 95

45

169

	gca gat gaa cta agg tca gat aca att ttc aat gta tca aag act ggg	336
	Ala Asp, Glu Leu Arg Ser Asp Thr Ile Phe Asn Val Ser Lys Thr Gly	
	100 105 110	
5	ggc cac ctt ggc tca agt ctt ggt gtt gtt gag ctg act gtt gct ctt	384
	Gly His Leu Gly Ser Ser Leu Gly Val Val Glu Leu Thr Val Ala Leu	
	115 120 125	
10	cat tat gtc ttc aat gca ccg caa gat agg att ctc tgg gat gtt ggt	432
	His Tyr Val Phe Asn Ala Pro Gln Asp Arg Ile Leu Trp Asp Val Gly	
	130 135 140	
15	cat cag tct tat cct cac aaa atc ttg act ggt aga agg gac aag atg	480
	His Gln Ser Tyr Pro His Lys Ile Leu Thr Gly Arg Arg Asp Lys Met	
	145 150 155 160	
20	tcg aca tta agg cag aca gat ggt ctt gca gga ttt act aag cga tcg	528
	Ser Thr Leu Arg Gln Thr Asp Gly Leu Ala Gly Phe Thr Lys Arg Ser	
	165 170 175	
	gag agt gaa tat gat tgc ttt ggc acc ggc cac agt tcc acc acc atc	576
	Glu Ser Glu Tyr Asp Cys Phe Gly Thr Gly His Ser Ser Thr Thr Ile	
	180 185 190	
25	tca gca ggc cta ggg atg gct gtt ggt aga gat cta aaa gga aga aac	624
	Ser Ala Gly Leu Gly Met Ala Val Gly Arg Asp Leu Lys Gly Arg Asn	
	195 200 205	
30	aac aat gtt att gcc gta ata ggt gat ggt gcc atg aca gca ggt caa	672
	Asn Asn Val Ile Ala Val Ile Gly Asp Gly Ala Met Thr Ala Gly Gln	
	210 215 220	
35	gct tat gaa gcc atg aat aat gct ggt tac ctg gac tct gac atg att	720
	Ala Tyr Glu Ala Met Asn Asn Ala Gly Tyr Leu Asp Ser Asp Met Ile	
	225 230 235 240	
40	gtt atc tta aac gac aat aga caa gtt tct tta cct act gct act ctg	768
	Val Ile Leu Asn Asp Asn Arg Gln Val Ser Leu Pro Thr Ala Thr Leu	
	245 250 255	
	gat ggg cca gtt gct cct gtt gga gct cta agt agt gct ttg agc agg	816
	Asp Gly Pro Val Ala Pro Val Gly Ala Leu Ser Ser Ala Leu Ser Arg	
	260 265 270	
45	tta cag tct aat agg cct ctc aga gaa cta aga gaa gtc gca aag gga	864

170

	Leu	Gln	Ser	Asn	Arg	Pro	Leu	Arg	Glu	Leu	Arg	Glu	Val	Ala	Lys	Gly		
	275						280						285					
5	gtt	act	aag	cag	att	ggt	ggt	cct	atg	cat	gag	ctt	gct	gca	aaa	ggt	912	
	Val	Thr	Lys	Gln	Ile	Gly	Gly	Pro	Met	His	Glu	Leu	Ala	Ala	Lys	Val		
	290					295					300							
10	gat	gaa	tat	gct	cgt	ggc	atg	att	agt	ggt	tct	gga	tca	aca	ttg	ttt	960	
	Asp	Glu	Tyr	Ala	Arg	Gly	Met	Ile	Ser	Gly	Ser	Gly	Ser	Thr	Leu	Phe		
	305					310					315					320		
15	gaa	gaa	ctt	gga	ctt	tac	tat	att	ggt	cct	gtg	gat	ggt	cac	aac	att	1008	
	Glu	Glu	Leu	Gly	Leu	Tyr	Tyr	Ile	Gly	Pro	Val	Asp	Gly	His	Asn	Ile		
				325					330					335				
20	gat	gat	cta	att	gcg	att	ctc	aaa	gag	ggt	aga	agt	act	aaa	aca	aca	1056	
	Asp	Asp	Leu	Ile	Ala	Ile	Leu	Lys	Glu	Val	Arg	Ser	Thr	Lys	Thr	Thr		
	340								345					350				
25	ggt	cca	gta	ctg	atc	cat	ggt	gtc	act	gag	aaa	ggc	aga	ggt	tat	cca	1104	
	Gly	Pro	Val	Leu	Ile	His	Val	Val	Thr	Glu	Lys	Gly	Arg	Gly	Tyr	Pro		
	355						360					365						
30	tat	gct	gag	aga	gct	gca	gat	aag	tat	cat	gga	ggt	gcc	aag	ttt	gat	1152	
	Tyr	Ala	Glu	Arg	Ala	Ala	Asp	Lys	Tyr	His	Gly	Val	Ala	Lys	Phe	Asp		
	370						375					380						
35	cca	gca	aca	gga	aag	caa	ttc	aaa	gcc	agt	gcc	aag	aca	cag	tcc	tat	1200	
	Pro	Ala	Thr	Gly	Lys	Gln	Phe	Lys	Ala	Ser	Ala	Lys	Thr	Gln	Ser	Tyr		
	385					390					395					400		
40	aca	aca	tat	ttt	gcc	gag	gct	tta	att	gca	gaa	gca	gaa	gca	gat	aaa	1248	
	Thr	Thr	Tyr	Phe	Ala	Glu	Ala	Leu	Ile	Ala	Glu	Ala	Glu	Ala	Asp	Lys		
				405					410					415				
45	gac	att	gtt	gca	atc	cat	gct	gcc	atg	ggg	ggt	ggg	acc	gga	atg	aac	1296	
	Asp	Ile	Val	Ala	Ile	His	Ala	Ala	Met	Gly	Gly	Gly	Thr	Gly	Met	Asn		
	420						425					430						
50	ctt	ttc	cat	cgt	cgc	ttc	cca	aca	agg	tgt	ttt	gat	gtt	gga	ata	gca	1344	
	Leu	Phe	His	Arg	Arg	Phe	Pro	Thr	Arg	Cys	Phe	Asp	Val	Gly	Ile	Ala		
	435						440					445						
55	gaa	caa	cat	gca	gta	acc	ttt	gct	gct	gga	ttg	gct	tgt	gaa	ggc	att	1392	
	Glu	Gln	His	Ala	Val	Thr	Phe	Ala	Ala	Gly	Leu	Ala	Cys	Glu	Gly	Ile		

	450	455	460	
	aaa cct ttc tgt gca atc tat tcg tct ttc atg cag agg gct tat gac			
	Lys Pro Phe Cys Ala Ile Tyr Ser Ser Phe Met Gln Arg Ala Tyr Asp			
5	465	470	475	480
	cag gta gtg cat gac gtt gat ttg caa aag ctg ccc gtg agg ttt gca			
	Gln Val Val His Asp Val Asp Leu Gln Lys Leu Pro Val Arg Phe Ala			
	485	490	495	
10	atg gac aga gca ggt ctt gtt gga gca gat ggt cca aca cat tgt ggt			
	Met Asp Arg Ala Gly Leu Val Gly Ala Asp Gly Pro Thr His Cys Gly			
	500	505	510	
15	gca ttt gat gtt act tac atg gca tgt ctt cdt aac atg gtt gta atg			
	Ala Phe Asp Val Thr Tyr Met Ala Cys Leu Pro Asn Met Val Val Met			
	515	520	525	
	gct cct tct gat gaa gcg gag cta ttt cac atg gta gca act gct gcc			
20	Ala Pro Ser Asp Glu Ala Glu Leu Phe His Met Val Ala Thr Ala Ala			
	530	535	540	
	gcc att gat gac aga cca agt tgt ttt aga tac cca aga gga aat ggg			
	Ala Ile Asp Asp Arg Pro Ser Cys Phe Arg Tyr Pro Arg Gly Asn Gly			
25	545	550	555	560
	atc ggt gta gag ctt ccg gct gga aac aaa gga att cct ctt gag gtt			
	Ile Gly Val Glu Leu Pro Ala Gly Asn Lys Gly Ile Pro Leu Glu Val			
	565	570	575	
30	ggt aaa ggt agg ata ttg att gag ggg gag aga gtg gct cta ttg gga			
	Gly Lys Gly Arg Ile Leu Ile Glu Gly Glu Arg Val Ala Leu Leu Gly			
	580	585	590	
35	tat ggc tca gca gtg cag aac tgt ttg gat gct gct att gtg cta gaa			
	Tyr Gly Ser Ala Val Gln Asn Cys Leu Asp Ala Ala Ile Val Leu Glu			
	595	600	605	
	tcc cgc ggc tta caa gta aca gtt gca gat gca cgt ttc tgc aaa cca			
40	Ser Arg Gly Leu Gln Val Thr Val Ala Asp Ala Arg Phe Cys Lys Pro			
	610	615	620	
	ctg gac cat gcc ctc ata agg agc ctt gca aaa tca cat gaa gtg cta			
	Leu Asp His Ala Leu Ile Arg Ser Leu Ala Lys Ser His Glu Val Leu			
45	625	630	635	640

5      atc act gtc gaa gaa gga tca att gga ggt ttt gga tct cat gtt gtt      1968  
       Ile Thr Val Glu Glu Gly Ser Ile Gly Gly Phe Gly Ser His Val Val  
                     645                      650                      655

10     cag ttc atg gcc tta gat ggg ctt ctt gat ggc aag ttg aag tgg aga      2016  
       Gln Phe Met Ala Leu Asp Gly Leu Leu Asp Gly Lys Leu Lys Trp Arg  
                     660                      665                      670

15     cca ata gtt ctt cct gat cga tac att gac cat gga tct cct gtt gat      2064  
       Pro Ile Val Leu Pro Asp Arg Tyr Ile Asp His Gly Ser Pro Val Asp  
                     675                      680                      685

20     cag ttg gcg gaa gct ggc cta aca cca tct cac att gca gca aca gta      2112  
       Gln Leu Ala Glu Ala Gly Leu Thr Pro Ser His Ile Ala Ala Thr Val  
                     690                      695                      700

25     ttt aac ata ctt gga caa acc aga gag gct cta gag gtc atg aca taa      2160  
       Phe Asn Ile Leu Gly Gln Thr Arg Glu Ala Leu Glu Val Met Thr  
       705                      710                      715

30     <210> 116

35     <211> 719

40     <212> PRT

45     <213> Lycopersicon esculentum

50     <400> 116

55     Met Ala Leu Cys Ala Tyr Ala Phe Pro Gly Ile Leu Asn Arg Thr Gly  
       1                      5                      10                      15

60     Val Val Ser Asp Ser Ser Lys Ala Thr Pro Leu Phe Ser Gly Trp Ile  
       20                      25                      30

65     His Gly Thr Asp Leu Gln Phe Leu Phe Gln His Lys Leu Thr His Glu  
       35                      40                      45



Val Lys Lys Arg Ser Arg Val Val Gln Ala Ser Leu Ser Glu Ser Gly  
 50 55 60

5

Glu Tyr Tyr Thr Gln Arg Pro Pro Thr Pro Ile Leu Asp Thr Val Asn  
 65 70 75 80

10

Tyr Pro Ile His Met Lys Asn Leu Ser Leu Lys Glu Leu Lys Gln Leu  
 85 90 95

15

Ala Asp Glu Leu Arg Ser Asp Thr Ile Phe Asn Val Ser Lys Thr Gly  
 100 105 110

20

Gly His Leu Gly Ser Ser Leu Gly Val Val Glu Leu Thr Val Ala Leu  
 115 120 125

25

His Tyr Val Phe Asn Ala Pro Gln Asp Arg Ile Leu Trp Asp Val Gly  
 130 135 140

30

His Gln Ser Tyr Pro His Lys Ile Leu Thr Gly Arg Arg Asp Lys Met  
 145 150 155 160

35

Ser Thr Leu Arg Gln Thr Asp Gly Leu Ala Gly Phe Thr Lys Arg Ser  
 165 170 175

40

Glu Ser Glu Tyr Asp Cys Phe Gly Thr Gly His Ser Ser Thr Thr Ile  
 180 185 190

45

Ser Ala Gly Leu Gly Met Ala Val Gly Arg Asp Leu Lys Gly Arg Asn  
 195 200 205

Asn Asn Val Ile Ala Val Ile Gly Asp Gly Ala Met Thr Ala Gly Gln  
 210 215 220

## 174

Ala Tyr Glu Ala Met Asn Asn Ala Gly Tyr Leu Asp Ser Asp Met Ile  
 225 230 235 240

5 Val Ile Leu Asn Asp Asn Arg Gln Val Ser Leu Pro Thr Ala Thr Leu  
 245 250 255

10 Asp Gly Pro Val Ala Pro Val Gly Ala Leu Ser Ser Ala Leu Ser Arg  
 260 265 270

15 Leu Gln Ser Asn Arg Pro Leu Arg Glu Leu Arg Glu Val Ala Lys Gly  
 275 280 285

Val Thr Lys Gln Ile Gly Gly Pro Met His Glu Leu Ala Ala Lys Val  
 290 295 300

20 Asp Glu Tyr Ala Arg Gly Met Ile Ser Gly Ser Gly Ser Thr Leu Phe  
 305 310 315 320

25 Glu Glu Leu Gly Leu Tyr Tyr Ile Gly Pro Val Asp Gly His Asn Ile  
 325 330 335

30 Asp Asp Leu Ile Ala Ile Leu Lys Glu Val Arg Ser Thr Lys Thr Thr  
 340 345 350

35 Gly Pro Val Leu Ile His Val Val Thr Glu Lys Gly Arg Gly Tyr Pro  
 355 360 365

Tyr Ala Glu Arg Ala Ala Asp Lys Tyr His Gly Val Ala Lys Phe Asp  
 370 375 380

40 Pro Ala Thr Gly Lys Gln Phe Lys Ala Ser Ala Lys Thr Gln Ser Tyr  
 385 390 395 400

45 Thr Thr Tyr Phe Ala Glu Ala Leu Ile Ala Glu Ala Glu Ala Asp Lys

175

405

410

415

5 Asp Ile Val Ala Ile His Ala Ala Met Gly Gly Gly Thr Gly Met Asn  
420 425 430

10 Leu Phe His Arg Arg Phe Pro Thr Arg Cys Phe Asp Val Gly Ile Ala  
435 440 445

15 Glu Gln His Ala Val Thr Phe Ala Ala Gly Leu Ala Cys Glu Gly Ile  
450 455 460

20 Lys Pro Phe Cys Ala Ile Tyr Ser Ser Phe Met Gln Arg Ala Tyr Asp  
465 470 475 480

25 Gln Val Val His Asp Val Asp Leu Gln Lys Leu Pro Val Arg Phe Ala  
485 490 495

30 Met Asp Arg Ala Gly Leu Val Gly Ala Asp Gly Pro Thr His Cys Gly  
500 505 510

35 Ala Phe Asp Val Thr Tyr Met Ala Cys Leu Pro Asn Met Val Val Met  
515 520 525

40 Ala Pro Ser Asp Glu Ala Glu Leu Phe His Met Val Ala Thr Ala Ala  
530 535 540

45 Ala Ile Asp Asp Arg Pro Ser Cys Phe Arg Tyr Pro Arg Gly Asn Gly  
545 550 555 560

50 Ile Gly Val Glu Leu Pro Ala Gly Asn Lys Gly Ile Pro Leu Glu Val  
565 570 575

55 Gly Lys Gly Arg Ile Leu Ile Glu Gly Glu Arg Val Ala Leu Leu Gly  
580 585 590

5 Tyr Gly Ser Ala Val Gln Asn Cys Leu Asp Ala Ala Ile Val Leu Glu  
595 600 605

10 Ser Arg Gly Leu Gln Val Thr Val Ala Asp Ala Arg Phe Cys Lys Pro  
610 615 620

15 Leu Asp His Ala Leu Ile Arg Ser Leu Ala Lys Ser His Glu Val Leu  
625 630 635 640

20 Gln Phe Met Ala Leu Asp Gly Leu Leu Asp Gly Lys Leu Lys Trp Arg  
660 665 670

25 Pro Ile Val Leu Pro Asp Arg Tyr Ile Asp His Gly Ser Pro Val Asp  
675 680 685

30 Gln Leu Ala Glu Ala Gly Leu Thr Pro Ser His Ile Ala Ala Thr Val  
690 695 700

35 Phe Asn Ile Leu Gly Gln Thr Arg Glu Ala Leu Glu Val Met Thr  
705 710 715

40 <210> 117.  
<211> 1434  
<212> DNA  
<213> Arabidopsis thaliana

&lt;220&gt;

&lt;221&gt; CDS

5 &lt;222&gt; (1)..(1434)

&lt;223&gt;

10

&lt;400&gt; 117

atg atg aca tta aac tca cta tct cca gct gaa tcc aaa gct att tct 48  
 Met Met Thr Leu Asn Ser Leu Ser Pro Ala Glu Ser Lys Ala Ile Ser

1 5 10 15

15

ttc ttg gat acc tcc agg ttc aat cca atc cct aaa ctc tca ggt ggg 96  
 Phe Leu Asp Thr Ser Arg Phe Asn Pro Ile Pro Lys Leu Ser Gly Gly

20 25 30

20

ttt agt ttg agg agg agg aat caa ggg aga ggt ttt gga aaa ggt gtt 144  
 Phe Ser Leu Arg Arg Arg Asn Gln Gly Arg Gly Phe Gly Lys Gly Val

35 40 45

25

aag tgt tca gtg aaa gtg cag cag caa caa caa cct cct cca gca tgg 192  
 Lys Cys Ser Val Lys Val Gln Gln Gln Gln Gln Pro Pro Pro Ala Trp

50 55 60

30

cct ggg aga gct gtc cct gag gcg cct cgt caa tct tgg gat gga cca 240  
 Pro Gly Arg Ala Val Pro Glu Ala Pro Arg Gln Ser Trp Asp Gly Pro

65 70 75 80

35

aaa ccc atc tct atc gtt gga tct act ggt tct att ggc act cag aca 288  
 Lys Pro Ile Ser Ile Val Gly Ser Thr Gly Ser Ile Gly Thr Gln Thr

85 90 95

ttg gat att gtg gct gag aat cct gac aaa ttc aga gtt gtg gct cta 336  
 Leu Asp Ile Val Ala Glu Asn Pro Asp Lys Phe Arg Val Val Ala Leu

100 105 110

40

gct gct ggt tcg aat gtt act cta ctt gct gat cag gta agg aga ttt 384  
 Ala Ala Gly Ser Asn Val Thr Leu Leu Ala Asp Gln Val Arg Arg Phe

115 120 125

45

aag cct gca ttg gtt gct gtt aga aac gag tca ctg att aat gag ctt 432  
 Lys Pro Ala Leu Val Ala Val Arg Asn Glu Ser Leu Ile Asn Glu Leu

	130	135	140	
	aaa gag gct tta gct gat ttg gac tat aaa ctc gag att att cca gga			480
	Lys Glu Ala Leu Ala Asp Leu Asp Tyr Lys Leu Glu Ile Ile Pro Gly			
5	145	150	155	160
	gag caa gga gtg att gag gtt gcc cga cat cct gaa gct gta acc gtt			528
	Glu Gln Gly Val Ile Glu Val Ala Arg His Pro Glu Ala Val Thr Val			
		165	170	175
10	gtt acc gga ata gta ggt tgt gcg gga cta aag cct acg gtt gct gca			576
	Val Thr Gly Ile Val Gly Cys Ala Gly Leu Lys Pro Thr Val Ala Ala			
		180	185	190
15	att gaa gca gga aag gac att gct ctt gca aac aaa gag aca tta atc			624
	Ile Glu Ala Gly Lys Asp Ile Ala Leu Ala Asn Lys Glu Thr Leu Ile			
		195	200	205
	gca ggt ggt cct ttc gtg ctt ccg ctt gcc aac aaa cat aat gta aag			672
20	Ala Gly Gly Pro Phe Val Leu Pro Leu Ala Asn Lys His Asn Val Lys			
		210	215	220
	att ctt ccg gca gat tca gaa cat tct gcc ata ttt cag tgt att caa			720
	Ile Leu Pro Ala Asp Ser Glu His Ser Ala Ile Phe Gln Cys Ile Gln			
25	225	230	235	240
	ggg ttg cct gaa ggc gct ctg cgc aag ata atc ttg act gca tct ggt			768
	Gly Leu Pro Glu Gly Ala Leu Arg Lys Ile Ile Leu Thr Ala Ser Gly			
		245	250	255
30	gga gct ttt agg gat tgg cct gtc gaa aag cta aag gaa gtt aaa gta			816
	Gly Ala Phe Arg Asp Trp Pro Val Glu Lys Leu Lys Glu Val Lys Val			
		260	265	270
35	gcg gat gcg ttg aag cat cca aac tgg aac atg gga aag aaa atc act			864
	Ala Asp Ala Leu Lys His Pro Asn Trp Asn Met Gly Lys Lys Ile Thr			
		275	280	285
	gtg gac tct gct acg ctt ttc aac aag ggt ctt gag gtc att gaa gcg			912
40	Val Asp Ser Ala Thr Leu Phe Asn Lys Gly Leu Glu Val Ile Glu Ala			
		290	295	300
	cat tat ttg ttt gga gct gag tat gac gat ata gag att gtc att cat			960
	His Tyr Leu Phe Gly Ala Glu Tyr Asp Asp Ile Glu Ile Val Ile His			
45	305	310	315	320

179

	ccg caa agt atc ata cat tcc atg att gaa aca cag gat tca tct gtg	1008
	Pro Gln Ser Ile Ile His Ser Met Ile Glu Thr Gln Asp Ser Ser Val	
	325 330 335	
5	ctt gct caa ttg ggt tgg cct gat atg cgt tta ccg att ctc tac acc	1056
	Leu Ala Gln Leu Gly Trp Pro Asp Met Arg Leu Pro Ile Leu Tyr Thr	
	340 345 350	
10	atg tca tgg ccc gat aga gtt cct tgt tct gaa gta act tgg cca aga	1104
	Met Ser Trp Pro Asp Arg Val Pro Cys Ser Glu Val Thr Trp Pro Arg	
	355 360 365	
15	ctt gac ctt tgc aaa ctc ggt tca ttg act ttc aag aaa cca gac aat	1152
	Leu Asp Leu Cys Lys Leu Gly Ser Leu Thr Phe Lys Lys Pro Asp Asn	
	370 375 380	
20	gtg aaa tac cca tcc atg gat ctt gct tat gct gct gga cga gct gga	1200
	Val Lys Tyr Pro Ser Met Asp Leu Ala Tyr Ala Ala Gly Arg Ala Gly	
	385 390 395 400	
25	ggc aca atg act gga gtt ctc agc gcc gcc aat gag aaa gct gtt gaa	1248
	Gly Thr Met Thr Gly Val Leu Ser Ala Ala Asn Glu Lys Ala Val Glu	
	405 410 415	
30	atg ttc att gat gaa aag ata agc tat ttg gat atc ttc aag gtt gtg	1296
	Met Phe Ile Asp Glu Lys Ile Ser Tyr Leu Asp Ile Phe Lys Val Val	
	420 425 430	
35	gaa tta aca tgc gat aaa cat cga aac gag ttg gta aca tca ccg tct	1344
	Glu Leu Thr Cys Asp Lys His Arg Asn Glu Leu Val Thr Ser Pro Ser	
	435 440 445	
40	ctt gaa gag att gtt cac tat gac ttg tgg gca cgt gaa tat gcc gcg	1392
	Leu Glu Glu Ile Val His Tyr Asp Leu Trp Ala Arg Glu Tyr Ala Ala	
	450 455 460	
40	aat gtg cag ctt tct tct ggt gct agg cca gtt cat gca tga	1434
	Asn Val Gln Leu Ser Ser Gly Ala Arg Pro Val His Ala	
	465 470 475	

&lt;210&gt; 118

&lt;211&gt; 477

&lt;212&gt; PRT

5 &lt;213&gt; Arabidopsis thaliana

&lt;400&gt; 118

10

Met Met Thr Leu Asn Ser Leu Ser Pro Ala Glu Ser Lys Ala Ile Ser  
 1 5 10 15

15

Phe Leu Asp Thr Ser Arg Phe Asn Pro Ile Pro Lys Leu Ser Gly Gly  
 20 25 30

20

Phe Ser Leu Arg Arg Arg Asn Gln Gly Arg Gly Phe Gly Lys Gly Val  
 35 40 45

25

Lys Cys Ser Val Lys Val Gln Gln Gln Gln Gln Pro Pro Pro Ala Trp  
 50 55 60

Pro Gly Arg Ala Val Pro Glu Ala Pro Arg Gln Ser Trp Asp Gly Pro  
 65 70 75 80

30

Lys Pro Ile Ser Ile Val Gly Ser Thr Gly Ser Ile Gly Thr Gln Thr  
 85 90 95

35

Leu Asp Ile Val Ala Glu Asn Pro Asp Lys Phe Arg Val Val Ala Leu  
 100 105 110

40

Ala Ala Gly Ser Asn Val Thr Leu Leu Ala Asp Gln Val Arg Arg Phe  
 115 120 125

45

Lys Pro Ala Leu Val Ala Val Arg Asn Glu Ser Leu Ile Asn Glu Leu  
 130 135 140



Lys Glu Ala Leu Ala Asp Leu Asp Tyr Lys Leu Glu Ile Ile Pro Gly  
 145 150 155 160

5

Glu Gln Gly Val Ile Glu Val Ala Arg His Pro Glu Ala Val Thr Val  
 165 170 175

10

Val Thr Gly Ile Val Gly Cys Ala Gly Leu Lys Pro Thr Val Ala Ala  
 180 185 190

15

Ile Glu Ala Gly Lys Asp Ile Ala Leu Ala Asn Lys Glu Thr Leu Ile  
 195 200 205

20

Ala Gly Gly Pro Phe Val Leu Pro Leu Ala Asn Lys His Asn Val Lys  
 210 215 220

25

Ile Leu Pro Ala Asp Ser Glu His Ser Ala Ile Phe Gln Cys Ile Gln  
 225 230 235 240

30

Gly Leu Pro Glu Gly Ala Leu Arg Lys Ile Ile Leu Thr Ala Ser Gly  
 245 250 255

35

Ala Asp Ala Leu Lys His Pro Asn Trp Asn Met Gly Lys Lys Ile Thr  
 275 280 285

40

Val Asp Ser Ala Thr Leu Phe Asn Lys Gly Leu Glu Val Ile Glu Ala  
 290 295 300

45

His Tyr Leu Phe Gly Ala Glu Tyr Asp Asp Ile Glu Ile Val Ile His  
 305 310 315 320

182

Pro Gln Ser Ile Ile His Ser Met Ile Glu Thr Gln Asp Ser Ser Val  
 325 330 335

5 Leu Ala Gln Leu Gly Trp Pro Asp Met Arg Leu Pro Ile Leu Tyr Thr  
 340 345 350

10 Met Ser Trp Pro Asp Arg Val Pro Cys Ser Glu Val Thr Trp Pro Arg  
 355 360 365

15 Leu Asp Leu Cys Lys Leu Gly Ser Leu Thr Phe Lys Lys Pro Asp Asn  
 370 375 380

20 Val Lys Tyr Pro Ser Met Asp Leu Ala Tyr Ala Ala Gly Arg Ala Gly  
 385 390 395 400

Gly Thr Met Thr Gly Val Leu Ser Ala Ala Asn Glu Lys Ala Val Glu  
 405 410 415

25 Met Phe Ile Asp Glu Lys Ile Ser Tyr Leu Asp Ile Phe Lys Val Val  
 420 425 430

30 Glu Leu Thr Cys Asp Lys His Arg Asn Glu Leu Val Thr Ser Pro Ser  
 435 440 445

35 Leu Glu Glu Ile Val His Tyr Asp Leu Trp Ala Arg Glu Tyr Ala Ala  
 450 455 460

Asn Val Gln Leu Ser Ser Gly Ala Arg Pro Val His Ala  
 465 470 475

40 <210> 119

<211> 884

&lt;212&gt; DNA

&lt;213&gt; Adonis palaestina clone ApIP128

5

&lt;220&gt;

&lt;221&gt; CDS

10

&lt;222&gt; (180)..(884)

&lt;223&gt;

15

&lt;400&gt; 119

cgtcgatcag gattaatcct ttatatagta tcttctccac caccactaaa acattatcag 60

20

cttcgtgttc ttctcccgtt gttcatcttc agcagcgttg tcgtactctt tctatttctt 120

cttccatcac taacagtcct cgccgaggggt tgaatcggtt gttcgcctca acgtcgact 179

25

atg ggt gaa gtc gct gat gct ggt atg gat gcc gtc cag aag cgg ctt 227

Met Gly Glu Val Ala Asp Ala Gly Met Asp Ala Val Gln Lys Arg Leu

1

5

10

15

atg ttc gac gat gaa tgt att ttg gtg gat gag aat gac aag gtc gtc 275

Met Phe Asp Asp Glu Cys Ile Leu Val Asp Glu Asn Asp Lys Val Val

30

20

25

30

gga cat gat tcc aaa tac aac tgt cat ttg atg gaa aag ata gag gca 323

Gly His Asp Ser Lys Tyr Asn Cys His Leu Met Glu Lys Ile Glu Ala

35

40

45

35

gaa aac ttg ctt cac aga gcc ttc agt gtt ttc tta ttc aac tca aaa 371

Glu Asn Leu Leu His Arg Ala Phe Ser Val Phe Leu Phe Asn Ser Lys

50

55

60

40

tac gag ttg ctt ctt cag caa cga tct gca acg aag gta aca ttc ccg 419

Tyr Glu Leu Leu Leu Gln Gln Arg Ser Ala Thr Lys Val Thr Phe Pro

65

70

75

80

45

ctc gta tgg aca aac acc tgt tgc agc cat ccc ctc ttc cgt gat tcc 467

Leu Val Trp Thr Asn Thr Cys Cys Ser His Pro Leu Phe Arg Asp Ser

5 gaa ctc ata gaa gaa aat ttt ctc ggg gta cga aac gct gca caa agg 515  
 Glu Leu Ile Glu Glu Asn Phe Leu Gly Val Arg Asn Ala Ala Gln Arg  
 100 105 110

10 aag ctt tta gac gag cta ggc att cca gct gaa gac gta cca gtt gat 563  
 Lys Leu Leu Asp Glu Leu Gly Ile Pro Ala Glu Asp Val Pro Val Asp  
 115 120 125

15 gaa ttc act cct ctt ggt cgc att ctt tao aaa gct cca tct gac gga 611  
 Glu Phe Thr Pro Leu Gly Arg Ile Leu Tyr Lys Ala Pro Ser Asp Gly  
 130 135 140

20 aaa tgg gga gag cac gaa ctg gac tat ctt ctg ttt att gtc cga gat 659  
 Lys Trp Gly Glu His Glu Leu Asp Tyr Leu Leu Phe Ile Val Arg Asp  
 145 150 155 160

25 gtg aaa tac gat cca aac cca gat gaa gtt gct gac gct aag tac gtt 707  
 Val Lys Tyr Asp Pro Asn Pro Asp Glu Val Ala Asp Ala Lys Tyr Val  
 165 170 175

30 aat cgc gag gag ttg aaa gag ata ctg aga aaa gct gat gca ggt gaa 755  
 Asn Arg Glu Glu Leu Lys Glu Ile Leu Arg Lys Ala Asp Ala Gly Glu  
 180 185 190

35 gag gga ata aag ttg tct cct tgg ttt aga ttg gtt gtg gat aac ttt 803  
 Glu Gly Ile Lys Leu Ser Pro Trp Phe Arg Leu Val Val Asp Asn Phe  
 195 200 205

40 ttg ttc aag tgg tgg gat cat gta gag gag ggg aag att aag gac gtc 851  
 Leu Phe Lys Trp Trp Asp His Val Glu Glu Gly Lys Ile Lys Asp Val  
 210 215 220

45 gcc gac atg aaa act atc cac aag ttg act taa 884  
 Ala Asp Met Lys Thr Ile His Lys Leu Thr  
 225 230

<210> 120  
 <211> 234  
 <212> PRT

&lt;213&gt; Adonis palaestina clone ApIP128

5 &lt;400&gt; 120

Met Gly Glu Val Ala Asp Ala Gly Met Asp Ala Val Gln Lys Arg Leu  
 1 5 10 15

10

Met Phe Asp Asp Glu Cys Ile Leu Val Asp Glu Asn Asp Lys Val Val  
 20 25 30

15

Gly His Asp Ser Lys Tyr Asn Cys His Leu Met Glu Lys Ile Glu Ala  
 35 40 45

20

Glu Asn Leu Leu His Arg Ala Phe Ser Val Phe Leu Phe Asn Ser Lys  
 50 55 60

25

Tyr Glu Leu Leu Leu Gln Gln Arg Ser Ala Thr Lys Val Thr Phe Pro  
 65 70 75 80

Leu Val Trp Thr Asn Thr Cys Cys Ser His Pro Leu Phe Arg Asp Ser  
 85 90 95

30

Glu Leu Ile Glu Glu Asn Phe Leu Gly Val Arg Asn Ala Ala Gln Arg  
 100 105 110

35

Lys Leu Leu Asp Glu Leu Gly Ile Pro Ala Glu Asp Val Pro Val Asp  
 115 120 125

40

Glu Phe Thr Pro Leu Gly Arg Ile Leu Tyr Lys Ala Pro Ser Asp Gly  
 130 135 140

45

Lys Trp Gly Glu His Glu Leu Asp Tyr Leu Leu Phe Ile Val Arg Asp  
 145 150 155 160

186

Val Lys Tyr Asp Pro Asn Pro Asp Glu Val Ala Asp Ala Lys Tyr Val  
165 170 175

5

Asn Arg Glu Glu Leu Lys Glu Ile Leu Arg Lys Ala Asp Ala Gly Glu  
180 185 190

10

Glu Gly Ile Lys Leu Ser Pro Trp Phe Arg Leu Val Val Asp Asn Phe  
195 200 205

15

Leu Phe Lys Trp Trp Asp His Val Glu Glu Gly Lys Ile Lys Asp Val  
210 215 220

20

Ala Asp Met Lys Thr Ile His Lys Leu Thr  
225 230

25

&lt;210&gt; 121

&lt;211&gt; 1402

&lt;212&gt; DNA

&lt;213&gt; Arabidopsis thaliana

30

&lt;220&gt;

&lt;221&gt; CDS

35

&lt;222&gt; (52)..(1317)

&lt;223&gt;

40

&lt;400&gt; 121

aagtctttgc ctctttgggtt tactttcctc tgttttcgat ccatttagaa a atg tta  
Met Leu

57

45

1

	ttc acg agg agt gtt gct cgg att tct tct aag ttt ctg aga aac cgt	105
	Phe Thr Arg Ser Val Ala Arg Ile Ser Ser Lys Phe Leu Arg Asn Arg	
	5 10 15	
5		
	agc ttc tat ggc tcc tct caa tct ctc gcc tct cat cgg ttc gca atc	153
	Ser Phe Tyr Gly Ser Ser Gln Ser Leu Ala Ser His Arg Phe Ala Ile	
	20 25 30	
10		
	att ccc gat cag ggt cac tct tgt tct gac tct cca cac aag ggt tac	201
	Ile Pro Asp Gln Gly His Ser Cys Ser Asp Ser Pro His Lys Gly Tyr	
	35 40 45 50	
15		
	gtt tgc aga aca act tat tca ttg aaa tct ccg gtt ttt ggt gga ttt	249
	Val Cys Arg Thr Thr Tyr Ser Leu Lys Ser Pro Val Phe Gly Gly Phe	
	55 60 65	
20		
	agt cat caa ctc tat cac cag agt agc tcc ttg gtt gag gag gag ctt	297
	Ser His Gln Leu Tyr His Gln Ser Ser Ser Leu Val Glu Glu Glu Leu	
	70 75 80	
25		
	gac cca ttt tcg ctt gtt gcc gat gag ctg tca ctt ctt agt aat aag	345
	Asp Pro Phe Ser Leu Val Ala Asp Glu Leu Ser Leu Leu Ser Asn Lys	
	85 90 95	
30		
	ttg aga gag atg gta ctt gcc gag gtt cca aag ctt gcc tct gct gct	393
	Leu Arg Glu Met Val Leu Ala Glu Val Pro Lys Leu Ala Ser Ala Ala	
	100 105 110	
35		
	gag tac ttc ttc aaa agg ggt gtg caa gga aaa cag ttt cgt tca act	441
	Glu Tyr Phe Phe Lys Arg Gly Val Gln Gly Lys Gln Phe Arg Ser Thr	
	115 120 125 130	
40		
	att ttg ctg ctg atg gcg aca gct ctg gat gta cga gtt cca gaa gca	489
	Ile Leu Leu Leu Met Ala Thr Ala Leu Asp Val Arg Val Pro Glu Ala	
	135 140 145	
45		
	ttg att ggg gaa tca aca gat ata gtc aca tca gaa tta cgc gta agg	537
	Leu Ile Gly Glu Ser Thr Asp Ile Val Thr Ser Glu Leu Arg Val Arg	
	150 155 160	
50		
	caa cgg ggt att gct gaa atc act gaa atg ata cac gtc gca agt cta	585
	Gln Arg Gly Ile Ala Glu Ile Thr Glu Met Ile His Val Ala Ser Leu	
	165 170 175	

188

	ctg cac gat gat gtc ttg gat gat gcc gat aca agg cgt ggt gtt ggt	633
	Leu His Asp Asp Val Leu Asp Asp Ala Asp Thr Arg Arg Gly Val Gly	
	180 185 190	
5	tcc tta aat gtt gta atg ggt aac aag atg tcg gta tta gca gga gac	681
	Ser Leu Asn Val Val Met Gly Asn Lys Met Ser Val Leu Ala Gly Asp	
	195 200 205 210	
10	ttc ttg ctc tcc cgg gct tgt ggg gct ctc gct gct tta aag aac aca	729
	Phe Leu Leu Ser Arg Ala Cys Gly Ala Leu Ala Ala Leu Lys Asn Thr	
	215 220 225	
15	gag gtt gta gca tta ctt gca act gct gta gaa cat ctt gtt acc ggt	777
	Glu Val Val Ala Leu Leu Ala Thr Ala Val Glu His Leu Val Thr Gly	
	230 235 240	
20	gaa acc atg gag ata act agt tca acc gag cag cgt tat agt atg gac	825
	Glu Thr Met Glu Ile Thr Ser Ser Thr Glu Gln Arg Tyr Ser Met Asp	
	245 250 255	
25	tac tac atg cag aag aca tat tat aag aca gca tcg cta atc tct aac	873
	Tyr Tyr Met Gln Lys Thr Tyr Tyr Lys Thr Ala Ser Leu Ile Ser Asn	
	260 265 270	
30	agc tgc aaa gct gtt gcc gtt ctc act gga caa aca gca gaa gtt gcc	921
	Ser Cys Lys Ala Val Ala Val Leu Thr Gly Gln Thr Ala Glu Val Ala	
	275 280 285 290	
35	gtg tta gct ttt gag tat ggg agg aat ctg ggt tta gca ttc caa tta	969
	Val Leu Ala Phe Glu Tyr Gly Arg Asn Leu Gly Leu Ala Phe Gln Leu	
	295 300 305	
40	ata gac gac att ctt gat ttc acg ggc aca tct gcc tct ctc gga aag	1017
	Ile Asp Asp Ile Leu Asp Phe Thr Gly Thr Ser Ala Ser Leu Gly Lys	
	310 315 320	
45	gga tcg ttg tca gat att cgc cat gga gtc ata aca gcc cca atc ctc	1065
	Gly Ser Leu Ser Asp Ile Arg His Gly Val Ile Thr Ala Pro Ile Leu	
	325 330 335	
50	ttt gcc atg gaa gag ttt cct caa cta cgc gaa gtt gtt gat caa gtt	1113
	Phe Ala Met Glu Glu Phe Pro Gln Leu Arg Glu Val Val Asp Gln Val	
	340 345 350	
55	gaa aaa gat cct agg aat gtt gac att gct tta gag tat ctt ggg aag	1161



189

Glu Lys Asp Pro Arg Asn Val Asp Ile Ala Leu Glu Tyr Leu Gly Lys  
 355 360 365 370

5 agc aag gga ata cag agg gca aga gaa tta gcc atg gaa cat gcg aat 1209  
 Ser Lys Gly Ile Gln Arg Ala Arg Glu Leu Ala Met Glu His Ala Asn  
 375 380 385

10 cta gca gca gct gca atc ggg tct cta cct gaa aca gac aat gaa gat 1257  
 Leu Ala Ala Ala Ala Ile Gly Ser Leu Pro Glu Thr Asp Asn Glu Asp  
 390 395 400

15 gtc aaa aga tcg agg cgg gca ctt att gac ttg acc cat aga gtc atc 1305  
 Val Lys Arg Ser Arg Arg Ala Leu Ile Asp Leu Thr His Arg Val Ile  
 405 410 415

acc aga aac aag tgagattaag taatgtttct ctctatacac caaaacattc 1357  
 Thr Arg Asn Lys  
 420

20 ctcatctcat ttgtaggatt ttgttggtcc aattcgtttc acgaa 1402

<210> 122

25 <211> 422

<212> PRT

30 <213> Arabidopsis thaliana

<400> 122

35 Met Leu Phe Thr Arg Ser Val Ala Arg Ile Ser Ser Lys Phe Leu Arg  
 1 5 10 15

40 Asn Arg Ser Phe Tyr Gly Ser Ser Gln Ser Leu Ala Ser His Arg Phe  
 20 25 30

45 Ala Ile Ile Pro Asp Gln Gly His Ser Cys Ser Asp Ser Pro His Lys  
 35 40 45

190

Gly Tyr Val Cys Arg Thr Thr Tyr Ser Leu Lys Ser Pro Val Phe Gly  
 50 55 60

5

Gly Phe Ser His Gln Leu Tyr His Gln Ser Ser Ser Leu Val Glu Glu  
 65 70 75 80

10

Glu Leu Asp Pro Phe Ser Leu Val Ala Asp Glu Leu Ser Leu Leu Ser  
 85 90 95

15

Asn Lys Leu Arg Glu Met Val Leu Ala Glu Val Pro Lys Leu Ala Ser  
 100 105 110

20

Ala Ala Glu Tyr Phe Phe Lys Arg Gly Val Gln Gly Lys Gln Phe Arg  
 115 120 125

Ser Thr Ile Leu Leu Leu Met Ala Thr Ala Leu Asp Val Arg Val Pro  
 130 135 140

25

Glu Ala Leu Ile Gly Glu Ser Thr Asp Ile Val Thr Ser Glu Leu Arg  
 145 150 155 160

30

Val Arg Gln Arg Gly Ile Ala Glu Ile Thr Glu Met Ile His Val Ala  
 165 170 175

35

Ser Leu Leu His Asp Asp Val Leu Asp Asp Ala Asp Thr Arg Arg Gly  
 180 185 190

40

Val Gly Ser Leu Asn Val Val Met Gly Asn Lys Met Ser Val Leu Ala  
 195 200 205

Gly Asp Phe Leu Leu Ser Arg Ala Cys Gly Ala Leu Ala Ala Leu Lys  
 210 215 220

45

•

• •

•

•

•

•

30

35

Gly Lys Ser Lys Gly Ile Gln Arg Ala Arg Glu Leu Ala Met Glu His

40

45

Val Ile Thr Arg Asn Lys

5

420

&lt;210&gt; 123

10

&lt;211&gt; 1155

&lt;212&gt; DNA

&lt;213&gt; Arabidopsis thaliana

15

&lt;220&gt;

20

&lt;221&gt; CDS

&lt;222&gt; (1)..(1155)

&lt;223&gt;

25

&lt;400&gt; 123

30

atg agt gtg agt tgt tgt tgt agg aat ctg ggc aag aca ata aaa aag

48

Met Ser Val Ser Cys Cys Cys Arg Asn Leu Gly Lys Thr Ile Lys Lys

1

5

10

15

gca ata cct tca cat cat ttg cat ctg aga agt ctt ggt ggg agt ctc

96

Ala Ile Pro Ser His His Leu His Leu Arg Ser Leu Gly Gly Ser Leu

35

20

25

30

tat cgt cgt cgt atc caa agc tct tca atg gag acc gat ctc aag tca

144

Tyr Arg Arg Arg Ile Gln Ser Ser Ser Met Glu Thr Asp Leu Lys Ser

35

40

45

40

acc ttt ctc aac gtt tat tct gtt ctc aag tct gac ctt ctt cat gac

192

Thr Phe Leu Asn Val Tyr Ser Val Leu Lys Ser Asp Leu Leu His Asp

50

55

60

45

cct tcc ttc gaa ttc acc aat gaa tct cgt ctc tgg gtt gat cgg atg

240

## 193

	Pro	Ser	Phe	Glu	Phe	Thr	Asn	Glu	Ser	Arg	Leu	Trp	Val	Asp	Arg	Met	
	65					70					75					80	
	ctg	gac	tac	aat	gta	cgt	gga	ggg	aaa	ctc	aat	cgg	ggg	ctc	tct	gtt	288
5	Leu	Asp	Tyr	Asn	Val	Arg	Gly	Gly	Lys	Leu	Asn	Arg	Gly	Leu	Ser	Val	
				85						90				95			
	gtt	gac	agt	ttc	aaa	ctt	ttg	aag	caa	ggc	aat	gat	ttg	act	gag	caa	336
10	Val	Asp	Ser	Phe	Lys	Leu	Leu	Lys	Gln	Gly	Asn	Asp	Leu	Thr	Glu	Gln	
				100					105					110			
	gag	gtt	ttc	ctc	tct	tgt	gct	ctc	ggg	tgg	tgc	att	gaa	tgg	ctc	caa	384
	Glu	Val	Phe	Leu	Ser	Cys	Ala	Leu	Gly	Trp	Cys	Ile	Glu	Trp	Leu	Gln	
			115					120					125				
15	gct	tat	ttc	ctt	gtg	ctt	gat	gat	att	atg	gat	aac	tct	gtc	act	cgc	432
	Ala	Tyr	Phe	Leu	Val	Leu	Asp	Asp	Ile	Met	Asp	Asn	Ser	Val	Thr	Arg	
		130					135				140						
20	cgt	ggg	caa	cct	tgc	tgg	ttc	aga	gtt	cct	cag	gtt	ggg	atg	gtt	gcc	480
	Arg	Gly	Gln	Pro	Cys	Trp	Phe	Arg	Val	Pro	Gln	Val	Gly	Met	Val	Ala	
	145				150					155					160		
	atc	aat	gat	ggg	att	cta	ctt	cgc	aat	cac	atc	cac	agg	att	ctc	aaa	528
25	Ile	Asn	Asp	Gly	Ile	Leu	Leu	Arg	Asn	His	Ile	His	Arg	Ile	Leu	Lys	
				165					170					175			
	aag	cat	ttc	cgt	gat	aag	cct	tac	tat	gtt	gac	ctt	gtt	gat	ttg	ttt	576
30	Lys	His	Phe	Arg	Asp	Lys	Pro	Tyr	Tyr	Val	Asp	Leu	Val	Asp	Leu	Phe	
			180					185					190				
	aat	gag	gtt	gag	ttg	caa	aca	gct	tgt	ggc	cag	atg	ata	gat	ttg	atc	624
	Asn	Glu	Val	Glu	Leu	Gln	Thr	Ala	Cys	Gly	Gln	Met	Ile	Asp	Leu	Ile	
		195					200				205						
35	acc	acc	ttt	gaa	gga	gaa	aag	gat	ttg	gcc	aag	tac	tca	ttg	tca	atc	672
	Thr	Thr	Phe	Glu	Gly	Glu	Lys	Asp	Leu	Ala	Lys	Tyr	Ser	Leu	Ser	Ile	
		210					215				220						
40	cac	cgt	cgt	att	gtc	cag	tac	aaa	acg	gct	tat	tac	tca	ttt	tat	ctc	720
	His	Arg	Arg	Ile	Val	Gln	Tyr	Lys	Thr	Ala	Tyr	Tyr	Ser	Phe	Tyr	Leu	
	225				230					235					240		
	cct	gtt	gct	tgt	gcg	ttg	ctt	atg	gcg	ggc	gaa	aat	ttg	gaa	aac	cat	768
45	Pro	Val	Ala	Cys	Ala	Leu	Leu	Met	Ala	Gly	Glu	Asn	Leu	Glu	Asn	His	

194

245

250

255

att gac gtg aaa aat gtt ctt gtt gac atg gga atc tac ttc caa gtg 816  
 Ile Asp Val Lys Asn Val Leu Val Asp Met Gly Ile Tyr Phe Gln Val  
 5 260 265 270  
 cag gat gat tat ctg gat tgt ttt gct gat ccc gag acg ctt ggc aag 864  
 Gln Asp Asp Tyr Leu Asp Cys Phe Ala Asp Pro Glu Thr Leu Gly Lys  
 275 280 285  
 10 ata gga aca gat ata gaa gat ttc aaa tgc tcg tgg ttg gtg gtt aag 912  
 Ile Gly Thr Asp Ile Glu Asp Phe Lys Cys Ser Trp Leu Val Val Lys  
 290 295 300  
 15 gca tta gag cgc tgc agc gaa gaa caa act aag ata tta tat gag aac 960  
 Ala Leu Glu Arg Cys Ser Glu Glu Gln Thr Lys Ile Leu Tyr Glu Asn  
 305 310 315 320  
 20 tat ggt aaa ccc gac cca tcg aac gtt gct aaa gtg aag gat ctc tac 1008  
 Tyr Gly Lys Pro Asp Pro Ser Asn Val Ala Lys Val Lys Asp Leu Tyr  
 325 330 335  
 aaa gag ctg gat ctt gag gga gtt ttc atg gag tat gag agc aaa agc 1056  
 Lys Glu Leu Asp Leu Glu Gly Val Phe Met Glu Tyr Glu Ser Lys Ser  
 25 340 345 350  
 tac gag aag ctg act gga gcg att gag gga cac caa agt aaa gca atc 1104  
 Tyr Glu Lys Leu Thr Gly Ala Ile Glu Gly His Gln Ser Lys Ala Ile  
 355 360 365  
 30 caa gca gtg cga aaa tcc ttc ttg gct aag atc tac aag agg cag aag 1152  
 Gln Ala Val Leu Lys Ser Phe Leu Ala Lys Ile Tyr Lys Arg Gln Lys  
 370 375 380  
 35 tag 1155

&lt;210&gt; 124

40 &lt;211&gt; 384

&lt;212&gt; PRT

45 <213> Arabidopsis thaliana

&lt;400&gt; 124

5 Met Ser Val Ser Cys Cys Cys Arg Asn Leu Gly Lys Thr Ile Lys Lys  
1 5 10 15

10 Ala Ile Pro Ser His His Leu His Leu Arg Ser Leu Gly Gly Ser Leu  
20 25 30

15 Tyr Arg Arg Arg Ile Gln Ser Ser Ser Met Glu Thr Asp Leu Lys Ser  
35 40 45

Thr Phe Leu Asn Val Tyr Ser Val Leu Lys Ser Asp Leu Leu His Asp  
50 55 60

20 Pro Ser Phe Glu Phe Thr Asn Glu Ser Arg Leu Trp Val Asp Arg Met  
65 70 75 80

25 Leu Asp Tyr Asn Val Arg Gly Gly Lys Leu Asn Arg Gly Leu Ser Val  
85 90 95

30 Val Asp Ser Phe Lys Leu Leu Lys Gln Gly Asn Asp Leu Thr Glu Gln  
100 105 110

35 Glu Val Phe Leu Ser Cys Ala Leu Gly Trp Cys Ile Glu Trp Leu Gln  
115 120 125

Ala Tyr Phe Leu Val Leu Asp Asp Ile Met Asp Asn Ser Val Thr Arg  
130 135 140

40 Arg Gly Gln Pro Cys Trp Phe Arg Val Pro Gln Val Gly Met Val Ala  
145 150 155 160

45 Ile Asn Asp Gly Ile Leu Leu Arg Asn His Ile His Arg Ile Leu Lys

5 Lys His Phe Arg Asp Lys Pro Tyr Tyr Val Asp Leu Val Asp Leu Phe  
180 185 190

10 Asn Glu Val Glu Leu Gln Thr Ala Cys Gly Gln Met Ile Asp Leu Ile  
195 200 205

Thr Thr Phe Glu Gly Glu Lys Asp Leu Ala Lys Tyr Ser Leu Ser Ile  
210 215 220

15 His Arg Arg Ile Val Gln Tyr Lys Thr Ala Tyr Tyr Ser Phe Tyr Leu  
225 230 235 240

20 Pro Val Ala Cys Ala Leu Leu Met Ala Gly Glu Asn Leu Glu Asn His  
245 250 255

25 Ile Asp Val Lys Asn Val Leu Val Asp Met Gly Ile Tyr Phe Gln Val  
260 265 270

30 Gln Asp Asp Tyr Leu Asp Cys Phe Ala Asp Pro Glu Thr Leu Gly Lys  
275 280 285

Ile Gly Thr Asp Ile Glu Asp Phe Lys Cys Ser Trp Leu Val Val Lys  
290 295 300

35 Ala Leu Glu Arg Cys Ser Glu Glu Gln Thr Lys Ile Leu Tyr Glu Asn  
305 310 315 320

40 Tyr Gly Lys Pro Asp Pro Ser Asn Val Ala Lys Val Lys Asp Leu Tyr  
325 330 335

45 Lys Glu Leu Asp Leu Glu Gly Val Phe Met Glu Tyr Glu Ser Lys Ser  
340 345 350



Tyr Glu Lys Leu Thr Gly Ala Ile Glu Gly His Gln Ser Lys Ala Ile  
 355 360 365  
 5

Gln Ala Val Leu Lys Ser Phe Leu Ala Lys Ile Tyr Lys Arg Gln Lys  
 370 375 380  
 10

<210> 125  
 <211> 1101  
 15 <212> DNA  
 <213> Sinabs alba

20  
 <220>  
 <221> CDS

25 <222> (1)..(1101)  
 <223>

30  
 <400> 125  
 atg gct tct tca gtg act cct cta ggt tca tgg gtt ctt ctt cac cat 48  
 Met Ala Ser Ser Val Thr Pro Leu Gly Ser Trp Val Leu Leu His His  
 1 5 10 15

35  
 cat cct tca act atc tta acc caa tcc aga tcc aga tct cct cct tct 96  
 His Pro Ser Thr Ile Leu Thr Gln Ser Arg Ser Arg Ser Pro Pro Ser  
 20 25 30

40  
 ctc atc acc ctt aaa ccc atc tcc ctc act cca aaa cgc acc gtt tcg 144  
 Leu Ile Thr Leu Lys Pro Ile Ser Leu Thr Pro Lys Arg Thr Val Ser  
 35 40 45

45  
 tct tct tcc tcc tct tcc ctc atc acc aaa gaa gac aac aac ctc aaa 192  
 Ser Ser Ser Ser Ser Ser Leu Ile Thr Lys Glu Asp Asn Asn Leu Lys

	50	55	60	
	tcc tct ttc tct tcc ttc gat ttc atg tct tac atc atc cgc aaa gcc			240
	Ser Ser Ser Ser Ser Phe Asp Phe Met Ser Tyr Ile Ile Arg Lys Ala			
5	65	70	75	80
	gac tcc gtc aac aaa gcc tta gac tcc gcc gtc cct ctc cgg gag cca			288
	Asp Ser Val Asn Lys Ala Leu Asp Ser Ala Val Pro Leu Arg Glu Pro			
	85	90	95	
10	ctc aag atc cac gaa gcg atg cgt tac tct ctc ctc gcc gga gga aaa			336
	Leu Lys Ile His Glu Ala Met Arg Tyr Ser Leu Leu Ala Gly Gly Lys			
	100	105	110	
15	cgc gtc aga cca gtt ctc tgc atc gcc gcg tgc gag cta gtc gga gga			384
	Arg Val Arg Pro Val Leu Cys Ile Ala Ala Cys Glu Leu Val Gly Gly			
	115	120	125	
	gaa gag tct tta gct atg ccg gcg cgt tgc gcc gtg gaa atg atc cac			432
20	Glu Glu Ser Leu Ala Met Pro Ala Arg Cys Ala Val Glu Met Ile His			
	130	135	140	
	acc atg tcg ttg atc cac gac gac ttg cct tgt atg gat aac gac gat			480
	Thr Met Ser Leu Ile His Asp Asp Leu Pro Cys Met Asp Asn Asp Asp			
25	145	150	155	160
	ctc cgc cgc gga aag ccc acg aat cac aaa gtt tac ggc gaa gac gtg			528
	Leu Arg Arg Gly Lys Pro Thr Asn His Lys Val Tyr Gly Glu Asp Val			
	165	170	175	
30	gcg gtt tta gcc gga gac gcg ctt ctt tcg ttc gcc ttc gag cat tta			576
	Ala Val Leu Ala Gly Asp Ala Leu Leu Ser Phe Ala Phe Glu His Leu			
	180	185	190	
35	gcg tcg gct acg agc tcg gag gtt tct ccg gcg aga gtg gtt aga gct			624
	Ala Ser Ala Thr Ser Ser Glu Val Ser Pro Ala Arg Val Val Arg Ala			
	195	200	205	
	gtg gga gag ttg gct aaa gcc atc ggc acc gaa ggg ctc gtg gcg gga			672
40	Val Gly Glu Leu Ala Lys Ala Ile Gly Thr Glu Gly Leu Val Ala Gly			
	210	215	220	
	caa gtg gtg gat ata agc agt gaa ggg ttg gac tta aac aac gtc gga			720
	Gln Val Val Asp Ile Ser Ser Glu Gly Leu Asp Leu Asn Asn Val Gly			
45	225	230	235	240

	ttg gag cat ttg aag ttt ata cat ttg cat aaa acg gcg gcg ttg ctt	768
	Leu Glu His Leu Lys Phe Ile His Leu His Lys Thr Ala Ala Leu Leu	
	245 250 255	
5		
	gaa gct tca gcg gtt ttg ggt ggg atc atc ggt gga ggg agt gat gaa	816
	Glu Ala Ser Ala Val Leu Gly Gly Ile Ile Gly Gly Gly Ser Asp Glu	
	260 265 270	
10		
	gag atc gag agg ctg agg aag ttc gcg agg tgt att ggg ttg ttg ttt	864
	Glu Ile Glu Arg Leu Arg Lys Phe Ala Arg Cys Ile Gly Leu Leu Phe	
	275 280 285	
15		
	cag gtg gtt gat gat atc ttg gac gtg acg aaa tcg tct caa gaa ctg	912
	Gln Val Val Asp Asp Ile Leu Asp Val Thr Lys Ser Ser Gln Glu Leu	
	290 295 300	
20		
	ggg aaa acc gct ggg aaa gat ttg att gct gat aag ttg act tat ccg	960
	Gly Lys Thr Ala Gly Lys Asp Leu Ile Ala Asp Lys Leu Thr Tyr Pro	
	305 310 315 320	
25		
	aag ctc atg ggt ttg gag aaa tcg aga gag ttc gct gag aag ttg aat	1008
	Lys Leu Met Gly Leu Glu Lys Ser Arg Glu Phe Ala Glu Lys Leu Asn	
	325 330 335	
30		
	aca gag gca cgt gat cag ctt tta ggg ttt gat tcc gac aag gtt gct	1056
	Thr Glu Ala Arg Asp Gln Leu Leu Gly Phe Asp Ser Asp Lys Val Ala	
	340 345 350	
35		
	cct ttg ttg gct ttg gct aat tac att gcc aat aga cag aac tga	1101
	Pro Leu Leu Ala Leu Ala Asn Tyr Ile Ala Asn Arg Gln Asn	
	355 360 365	
40		
	<210> 126	
	<211> 366	
	<212> PRT	
45		
	<213> Sinabs alba	
	<400> 126	

Met Ala Ser Ser Val Thr Pro Leu Gly Ser Trp Val Leu Leu His His  
 1 5 10 15  
 5  
 His Pro Ser Thr Ile Leu Thr Gln Ser Arg Ser Arg Ser Pro Pro Ser  
 20 25 30  
 10  
 Leu Ile Thr Leu Lys Pro Ile Ser Leu Thr Pro Lys Arg Thr Val Ser  
 35 40 45  
 15  
 Ser Ser Ser Ser Ser Ser Leu Ile Thr Lys Glu Asp Asn Asn Leu Lys  
 50 55 60  
 20  
 Ser Ser Ser Ser Ser Phe Asp Phe Met Ser Tyr Ile Ile Arg Lys Ala  
 65 70 75 80  
 Asp Ser Val Asn Lys Ala Leu Asp Ser Ala Val Pro Leu Arg Glu Pro  
 85 90 95  
 25  
 Leu Lys Ile His Glu Ala Met Arg Tyr Ser Leu Leu Ala Gly Gly Lys  
 100 105 110  
 30  
 Arg Val Arg Pro Val Leu Cys Ile Ala Ala Cys Glu Leu Val Gly Gly  
 115 120 125  
 35  
 Glu Glu Ser Leu Ala Met Pro Ala Arg Cys Ala Val Glu Met Ile His  
 130 135 140  
 40  
 Thr Met Ser Leu Ile His Asp Asp Leu Pro Cys Met Asp Asn Asp Asp  
 145 150 155 160  
 Leu Arg Arg Gly Lys Pro Thr Asn His Lys Val Tyr Gly Glu Asp Val  
 165 170 175  
 45

201

	Ala Val Leu Ala Gly Asp Ala Leu Leu Ser Phe Ala Phe Glu His Leu	
	180	185 190
5	Ala Ser Ala Thr Ser Ser Glu Val Ser Pro Ala Arg Val Val Arg Ala	
	195	200 205
10	Val Gly Glu Leu Ala Lys Ala Ile Gly Thr Glu Gly Leu Val Ala Gly	
	210	215 220
15	Gln Val Val Asp Ile Ser Ser Glu Gly Leu Asp Leu Asn Asn Val Gly	
	225	230 235 240
20	Leu Glu His Leu Lys Phe Ile His Leu His Lys Thr Ala Ala Leu Leu	
	245	250 255
25	Glu Ala Ser Ala Val Leu Gly Gly Ile Ile Gly Gly Gly Ser Asp Glu	
	260	265 270
30	Gln Val Val Asp Asp Ile Leu Asp Val Thr Lys Ser Ser Gln Glu Leu	
	290	295 300
35	Gly Lys Thr Ala Gly Lys Asp Leu Ile Ala Asp Lys Leu Thr Tyr Pro	
	305	310 315 320
40	Lys Leu Met Gly Leu Glu Lys Ser Arg Glu Phe Ala Glu Lys Leu Asn	
	325	330 335
45	Thr Glu Ala Arg Asp Gln Leu Leu Gly Phe Asp Ser Asp Lys Val Ala	
	340	345 350
50	Pro Leu Leu Ala Leu Ala Asn Tyr Ile Ala Asn Arg Gln Asn	

355

360

365

&lt;210&gt; 127

5

&lt;211&gt; 930

&lt;212&gt; DNA

10 &lt;213&gt; Erwinia uredovora

&lt;220&gt;

15

&lt;221&gt; CDS

&lt;222&gt; (1) .. (930)

20 &lt;223&gt;

&lt;400&gt; 127

25

atg aat aat ccg tcg tta ctc aat cat gcg gtc gaa acg atg gca gtt 48  
 Met Asn Asn Pro Ser Leu Leu Asn His Ala Val Glu Thr Met Ala Val  
 1 5 10 15

30

ggc tcg aaa agt ttt gcg aca gcc tca aag tta ttt gat gca aaa acc 96  
 Gly Ser Lys Ser Phe Ala Thr Ala Ser Lys Leu Phe Asp Ala Lys Thr  
 " 20 25 30

35

cgg cgc agc gta ctg atg ctc tac gcc tgg tgc cgc cat tgt gac gat 144  
 Arg Arg Ser Val Leu Met Leu Tyr Ala Trp Cys Arg His Cys Asp Asp  
 35 40 45

40

gtt att gac gat cag acg ctg ggc ttt cag gcc cgg cag cct gcc tta 192  
 Val Ile Asp Asp Gln Thr Leu Gly Phe Gln Ala Arg Gln Pro Ala Leu  
 50 55 60

caa acg ccc gaa caa cgt ctg atg caa ctt gag atg aaa acg cgc cag 240  
 Gln Thr Pro Glu Gln Arg Leu Met Gln Leu Glu Met Lys Thr Arg Gln  
 65 70 75 80

45

gcc tat gca gga tcg cag atg cac gaa ccg gcg ttt gcg gct ttt cag 288

	Ala Tyr Ala Gly Ser Gln Met His Glu Pro Ala Phe Ala Ala Phe Gln	
	85 90 95	
5	gaa gtg gct atg gct cat gat atc gcc ccg gct tac gcg ttt gat cat Glu Val Ala Met Ala His Asp Ile Ala Pro Ala Tyr Ala Phe Asp His	336
	100 105 110	
10	ctg gaa ggc ttc gcc atg gat gta cgc gaa gcg caa tac agc caa ctg Leu Glu Gly Phe Ala Met Asp Val Arg Glu Ala Gln Tyr Ser Gln Leu	384
	115 120 125	
15	gat gat acg ctg cgc tat tgc tat cac gtt gca ggc gtt gtc ggc ttg Asp Asp Thr Leu Arg Tyr Cys Tyr His Val Ala Gly Val Val Gly Leu	432
	130 135 140	
	atg atg gcg caa atc atg ggc gtg cgg gat aac gcc acg ctg gac cgc Met Met Ala Gln Ile Met Gly Val Arg Asp Asn Ala Thr Leu Asp Arg	480
	145 150 155 160	
20	gcc tgt gac ctt ggg ctg gca ttt cag ttg acc aat att gct cgc gat Ala Cys Asp Leu Gly Leu Ala Phe Gln Leu Thr Asn Ile Ala Arg Asp	528
	165 170 175	
25	att gtg gac gat gcg cat gcg ggc cgc tgt tat ctg ccg gca agc tgg Ile Val Asp Asp Ala His Ala Gly Arg Cys Tyr Leu Pro Ala Ser Trp	576
	180 185 190	
30	ctg gag cat gaa ggt ctg aac aaa gag aat tat gcg gca cct gaa aac Leu Glu His Glu Gly Leu Asn Lys Glu Asn Tyr Ala Ala Pro Glu Asn	624
	195 200 205	
35	cgt cag gcg ctg agc cgt atc gcc cgt cgt ttg gtg cag gaa gca gaa Arg Gln Ala Leu Ser Arg Ile Ala Arg Arg Leu Val Gln Glu Ala Glu	672
	210 215 220	
	cct tac tat ttg tct gcc aca gcc ggc ctg gca ggg ttg ccc ctg cgt Pro Tyr Tyr Leu Ser Ala Thr Ala Gly Leu Ala Gly Leu Pro Leu Arg	720
	225 230 235 240	
40	tcc gcc tgg gca atc gct acg gcg aag cag gtt tac cgg aaa ata ggt Ser Ala Trp Ala Ile Ala Thr Ala Lys Gln Val Tyr Arg Lys Ile Gly	768
	245 250 255	
45	gtc aaa gtt gaa cag gcc ggt cag caa gcc tgg gat cag cgg cag tca Val Lys Val Glu Gln Ala Gly Gln Gln Ala Trp Asp Gln Arg Gln Ser	816

204

	260	265	270	
	acg acc acg ccc gaa aaa tta acg ctg ctg ctg gcc gcc tct ggt cag			864
	Thr Thr Thr Pro Glu Lys Leu Thr Leu Leu Leu Ala Ala Ser Gly Gln			
5	275	280	285	
	gcc ctt act tcc cgg atg cgg gct cat cct ccc cgc cct gcg cat ctc			912
	Ala Leu Thr Ser Arg Met Arg Ala His Pro Pro Arg Pro Ala His Leu			
10	290	295	300	
	tgg cag cgc ccg ctc tag			930
	Trp Gln Arg Pro Leu			
	305			
15	<210> 128			
	<211> 309			
20	<212> PRT			
	<213> Erwinia uredovora			
25	<400> 128			
	Met Asn Asn Pro Ser Leu Leu Asn His Ala Val Glu Thr Met Ala Val			
	1 5 10 15			
30	Gly Ser Lys Ser Phe Ala Thr Ala Ser Lys Leu Phe Asp Ala Lys Thr			
	20 25 30			
35	Arg Arg Ser Val Leu Met Leu Tyr Ala Trp Cys Arg His Cys Asp Asp			
	35 40 45			
40	Val Ile Asp Asp Gln Thr Leu Gly Phe Gln Ala Arg Gln Pro Ala Leu			
	50 55 60			
45	Gln Thr Pro Glu Gln Arg Leu Met Gln Leu Glu Met Lys Thr Arg Gln			
	65 70 75 80			



Ala Tyr Ala Gly Ser Gln Met His Glu Pro Ala Phe Ala Ala Phe Gln  
 85 90 95  
 5

Glu Val Ala Met Ala His Asp Ile Ala Pro Ala Tyr Ala Phe Asp His  
 100 105 110

10

Leu Glu Gly Phe Ala Met Asp Val Arg Glu Ala Gln Tyr Ser Gln Leu  
 115 120 125

15

Asp Asp Thr Leu Arg Tyr Cys Tyr His Val Ala Gly Val Val Gly Leu  
 130 135 140

20

Met Met Ala Gln Ile Met Gly Val Arg Asp Asn Ala Thr Leu Asp Arg  
 145 150 155 160

25

Ala Cys Asp Leu Gly Leu Ala Phe Gln Leu Thr Asn Ile Ala Arg Asp  
 165 170 175

30

Ile Val Asp Asp Ala His Ala Gly Arg Cys Tyr Leu Pro Ala Ser Trp  
 180 185 190

35

Leu Glu His Glu Gly Leu Asn Lys Glu Asn Tyr Ala Ala Pro Glu Asn  
 195 200 205

40

Arg Gln Ala Leu Ser Arg Ile Ala Arg Arg Leu Val Gln Glu Ala Glu  
 210 215 220

45

Pro Tyr Tyr Leu Ser Ala Thr Ala Gly Leu Ala Gly Leu Pro Leu Arg  
 225 230 235 240

Ser Ala Trp Ala Ile Ala Thr Ala Lys Gln Val Tyr Arg Lys Ile Gly  
 245 250 255

Val Lys Val Glu Gln Ala Gly Gln Gln Ala Trp Asp Gln Arg Gln Ser  
 260 265 270

5 Thr Thr Thr Pro Glu Lys Leu Thr Leu Leu Leu Ala Ala Ser Gly Gln  
 275 280 285

10 Ala Leu Thr Ser Arg Met Arg Ala His Pro Pro Arg Pro Ala His Leu  
 290 295 300

15 Trp Gln Arg Pro Leu  
 305

<210> 129

20 <211> 1479

<212> DNA

<213> Erwinia uredovora

25

<220>

30 <221> CDS

<222> (1)..(1479)

<223>

35

<400> 129

40 atg aaa cca act acg gta att ggt gca ggc ttc ggt ggc ctg gca ctg 48  
 Met Lys Pro Thr Thr Val Ile Gly Ala Gly Phe Gly Gly Leu Ala Leu  
 1 5 10 15

45 gca att cgt cta caa gct gcg ggg atc ccc gtc tta ctg ctt gaa caa 96  
 Ala Ile Arg Leu Gln Ala Ala Gly Ile Pro Val Leu Leu Leu Glu Gln  
 20 25 30

	cgt gat aaa ccc ggc ggt cgg gct tat gtc tac gag gat cag ggg ttt	144
	Arg Asp Lys Pro Gly Gly Arg Ala Tyr Val Tyr Glu Asp Gln Gly Phe	
	35 40 45	
5	acc ttt gat gca ggc ccg acg gtt atc acc gat ccc agt gcc att gaa	192
	Thr Phe Asp Ala Gly Pro Thr Val Ile Thr Asp Pro Ser Ala Ile Glu	
	50 55 60	
10	gaa ctg ttt gca ctg gca gga aaa cag tta aaa gag tat gtc gaa ctg	240
	Glu Leu Phe Ala Leu Ala Gly Lys Gln Leu Lys Glu Tyr Val Glu Leu	
	65 70 75 80	
15	ctg ccg gtt acg ccg ttt tac cgc ctg tgt tgg gag tca ggg aag gtc	288
	Leu Pro Val Thr Pro Phe Tyr Arg Leu Cys Trp Glu Ser Gly Lys Val	
	85 90 95	
20	ttt aat tac gat aac gat caa acc cgg ctc gaa gcg cag att cag cag	336
	Phe Asn Tyr Asp Asn Asp Gln Thr Arg Leu Glu Ala Gln Ile Gln Gln	
	100 105 110	
25	ttt aat ccc cgc gat gtc gaa ggt tat cgt cag ttt ctg gac tat tca	384
	Phe Asn Pro Arg Asp Val Glu Gly Tyr Arg Gln Phe Leu Asp Tyr Ser	
	115 120 125	
30	cgc gcg gtg ttt aaa gaa ggc tat cta aag ctc ggt act gtc cct ttt	432
	Arg Ala Val Phe Lys Glu Gly Tyr Leu Lys Leu Gly Thr Val Pro Phe	
	130 135 140	
35	tta tcg ttc aga gac atg ctt cgc gcc gca cct caa ctg gcg aaa ctg	480
	Leu Ser Phe Arg Asp Met Leu Arg Ala Ala Pro Gln Leu Ala Lys Leu	
	145 150 155 160	
40	cag gca tgg aga agc gtt tac agt aag gtt gcc agt tac atc gaa gat	528
	Gln Ala Trp Arg Ser Val Tyr Ser Lys Val Ala Ser Tyr Ile Glu Asp	
	165 170 175	
45	gaa cat ctg cgc cag gcg ttt tct ttc cac tcg ctg ttg gtg ggc ggc	576
	Glu His Leu Arg Gln Ala Phe Ser Phe His Ser Leu Leu Val Gly Gly	
	180 185 190	
50	aat ccc ttc gcc acc tca tcc att tat acg ttg ata cac gcg ctg gag	624
	Asn Pro Phe Ala Thr Ser Ser Ile Tyr Thr Leu Ile His Ala Leu Glu	
	195 200 205	

208

	cgt gag tgg ggc gtc tgg ttt ccg cgt ggc ggc acc ggc gca tta gtt	672
	Arg Glu Trp Gly Val Trp Phe Pro Arg Gly Gly Thr Gly Ala Leu Val	
	210 215 220	
5	cag ggg atg ata aag ctg ttt cag gat ctg ggt ggc gaa gtc gtg tta	720
	Gln Gly Met Ile Lys Leu Phe Gln Asp Leu Gly Gly Glu Val Val Leu	
	225 230 235 240	
	aac gcc aga gtc agc cat atg gaa acg aca gga aac aag att gaa gcc	768
10	Asn Ala Arg Val Ser His Met Glu Thr Thr Gly Asn Lys Ile Glu Ala	
	245 250 255	
	gtg cat tta gag gac ggt cgc agg ttc ctg acg caa gcc gtc gcg tca	816
	Val His Leu Glu Asp Gly Arg Arg Phe Leu Thr Gln Ala Val Ala Ser	
15	260 265 270	
	aat gca gat gtg gtt cat acc tat cgc gac ctg tta agc cag cac cct	864
	Asn Ala Asp Val Val His Thr Tyr Arg Asp Leu Leu Ser Gln His Pro	
	275 280 285	
20	gcc gcg gtt aag cag tcc aac aaa ctg cag act aag cgc atg agt aac	912
	Ala Ala Val Lys Gln Ser Asn Lys Leu Gln Thr Lys Arg Met Ser Asn	
	290 295 300	
25	tct ctg ttt gtg ctc tat ttt ggt ttg aat cac cat cat gat cag ctc	960
	Ser Leu Phe Val Leu Tyr Phe Gly Leu Asn His His His Asp Gln Leu	
	305 310 315 320	
	gcg cat cac acg gtt tgt ttc ggc ccg cgt tac cgc gag ctg att gac	1008
30	Ala His His Thr Val Cys Phe Gly Pro Arg Tyr Arg Glu Leu Ile Asp	
	325 330 335	
	gaa att ttt aat cat gat ggc ctc gca gag gac ttc tca ctt tat ctg	1056
	Glu Ile Phe Asn His Asp Gly Leu Ala Glu Asp Phe Ser Leu Tyr Leu	
35	340 345 350	
	cac gcg ccc tgt gtc acg gat tcg tca ctg gcg cct gaa ggt tgc ggc	1104
	His Ala Pro Cys Val Thr Asp Ser Ser Leu Ala Pro Glu Gly Cys Gly	
	355 360 365	
40	agt tac tat gtg ttg gcg ccg gtg ccg cat tta ggc acc gcg aac ctc	1152
	Ser Tyr Tyr Val Leu Ala Pro Val Pro His Leu Gly Thr Ala Asn Leu	
	370 375 380	
45	gac tgg acg gtt gag ggg cca aaa cta cgc gac cgt att ttt gcg tac	1200

## 209

	Asp	Trp	Thr	Val	Glu	Gly	Pro	Lys	Leu	Arg	Asp	Arg	Ile	Phe	Ala	Tyr	
	385						390					395				400	
5	ctt	gag	cag	cat	tac	atg	cct	ggc	tta	cgg	agt	cag	ctg	gtc	acg	cac	1248
	Leu	Glu	Gln	His	Tyr	Met	Pro	Gly	Leu	Arg	Ser	Gln	Leu	Val	Thr	His	
					405					410					415		
10	cgg	atg	ttt	acg	ccg	ttt	gat	ttt	cgc	gac	cag	ctt	aat	gcc	tat	cat	1296
	Arg	Met	Phe	Thr	Pro	Phe	Asp	Phe	Arg	Asp	Gln	Leu	Asn	Ala	Tyr	His	
				420					425					430			
15	ggc	tca	gcc	ttt	tct	gtg	gag	ccc	gtt	ctt	acc	cag	agc	gcc	tgg	ttt	1344
	Gly	Ser	Ala	Phe	Ser	Val	Glu	Pro	Val	Leu	Thr	Gln	Ser	Ala	Trp	Phe	
				435				440						445			
20	cgg	ccg	cat	aac	cgc	gat	aaa	acc	att	act	aat	ctc	tac	ctg	gtc	ggc	1392
	Arg	Pro	His	Asn	Arg	Asp	Lys	Thr	Ile	Thr	Asn	Leu	Tyr	Leu	Val	Gly	
				450				455						460			
25	gca	ggc	acg	cat	ccc	ggc	gca	ggc	att	cct	ggc	gtc	atc	ggc	tcg	gca	1440
	Ala	Gly	Thr	His	Pro	Gly	Ala	Gly	Ile	Pro	Gly	Val	Ile	Gly	Ser	Ala	
						470					475					480	
30	aaa	gcg	aca	gca	ggc	ttg	atg	ctg	gag	gat	ctg	ata	tga				1479
	Lys	Ala	Thr	Ala	Gly	Leu	Met	Leu	Glu	Asp	Leu	Ile					
					485					490							
35	<210>																
40	<211>	"															
	<212>																
45	<213>																
	<400>																
	Met	Lys	Pro	Thr	Thr	Val	Ile	Gly	Ala	Gly	Phe	Gly	Gly	Leu	Ala	Leu	
	1					5				10					15		
50	Ala	Ile	Arg	Leu	Gln	Ala	Ala	Gly	Ile	Pro	Val	Leu	Leu	Leu	Glu	Gln	

20

25

30

5 Arg Asp Lys Pro Gly Gly Arg Ala Tyr Val Tyr Glu Asp Gln Gly Phe  
 35 40 45

10 Thr Phe Asp Ala Gly Pro Thr Val Ile Thr Asp Pro Ser Ala Ile Glu  
 50 55 60

15 Glu Leu Phe Ala Leu Ala Gly Lys Gln Leu Lys Glu Tyr Val Glu Leu  
 65 70 75 80

20 Leu Pro Val Thr Pro Phe Tyr Arg Leu Cys Trp Glu Ser Gly Lys Val  
 85 90 95

25 Phe Asn Tyr Asp Asn Asp Gln Thr Arg Leu Glu Ala Gln Ile Gln Gln  
 100 105 110

30 Phe Asn Pro Arg Asp Val Glu Gly Tyr Arg Gln Phe Leu Asp Tyr Ser  
 115 120 125

35 Arg Ala Val Phe Lys Glu Gly Tyr Leu Lys Leu Gly Thr Val Pro Phe  
 130 135 140

40 Leu Ser Phe Arg Asp Met Leu Arg Ala Ala Pro Gln Leu Ala Lys Leu  
 145 150 155 160

45 Gln Ala Trp Arg Ser Val Tyr Ser Lys Val Ala Ser Tyr Ile Glu Asp  
 165 170 175

50 Glu His Leu Arg Gln Ala Phe Ser Phe His Ser Leu Leu Val Gly Gly  
 180 185 190

55 Asn Pro Phe Ala Thr Ser Ser Ile Tyr Thr Leu Ile His Ala Leu Glu  
 195 200 205

Arg Glu Trp Gly Val Trp Phe Pro Arg Gly Gly Thr Gly Ala Leu Val  
 210 215 220  
 5

Gln Gly Met Ile Lys Leu Phe Gln Asp Leu Gly Gly Glu Val Val Leu  
 225 230 235 240

10

Asn Ala Arg Val Ser His Met Glu Thr Thr Gly Asn Lys Ile Glu Ala  
 245 250 255

15

Val His Leu Glu Asp Gly Arg Arg Phe Leu Thr Gln Ala Val Ala Ser  
 260 265 270

20

Asn Ala Asp Val Val His Thr Tyr Arg Asp Leu Leu Ser Gln His Pro  
 275 280 285

25

Ala Ala Val Lys Gln Ser Asn Lys Leu Gln Thr Lys Arg Met Ser Asn  
 290 295 300

30

Ser Leu Phe Val Leu Tyr Phe Gly Leu Asn His His His Asp Gln Leu  
 305 310 315 320

35

Glu Ile Phe Asn His Asp Gly Leu Ala Glu Asp Phe Ser Leu Tyr Leu  
 340 345 350

40

His Ala Pro Cys Val Thr Asp Ser Ser Leu Ala Pro Glu Gly Cys Gly  
 355 360 365

45

Ser Tyr Tyr Val Leu Ala Pro Val Pro His Leu Gly Thr Ala Asn Leu  
 370 375 380

Asp Trp Thr Val Glu Gly Pro Lys Leu Arg Asp Arg Ile Phe Ala Tyr  
 385 390 395 400

5

Leu Glu Gln His Tyr Met Pro Gly Leu Arg Ser Gln Leu Val Thr His  
 405 410 415

10

Arg Met Phe Thr Pro Phe Asp Phe Arg Asp Gln Leu Asn Ala Tyr His  
 420 425 430

15

Gly Ser Ala Phe Ser Val Glu Pro Val Leu Thr Gln Ser Ala Trp Phe  
 435 440 445

20

Arg Pro His Asn Arg Asp Lys Thr Ile Thr Asn Leu Tyr Leu Val Gly  
 450 455 460

Ala Gly Thr His Pro Gly Ala Gly Ile Pro Gly Val Ile Gly Ser Ala  
 465 470 475 480

25

Lys Ala Thr Ala Gly Leu Met Leu Glu Asp Leu Ile  
 485 490

30

<210> 131

<211> 1725

<212> DNA

35

<213> Narcissus pseudonarcissus

40

<220>

<221> CDS

<222> (1)..(1725)

45



&lt;223&gt;

5 &lt;400&gt; 131

atg gct tct tcc act tgt tta att cat tct tcc tct ttt ggg gtt gga 48  
 Met Ala Ser Ser Thr Cys Leu Ile His Ser Ser Ser Phe Gly Val Gly  
 1 5 10 15

10 gga aag aaa gtg aag atg aac acg atg att cga tgc aag ttg ttt tca 96  
 Gly Lys Lys Val Lys Met Asn Thr Met Ile Arg Ser Lys Leu Phe Ser  
 20 25 30

15 att cgg tgc gct ttg gac act aag gtg tct gat atg agc gtc aat gct 144  
 Ile Arg Ser Ala Leu Asp Thr Lys Val Ser Asp Met Ser Val Asn Ala  
 35 40 45

20 cca aaa gga ttg ttt cca cca gag cct gag cac tac agg ggg cca aag 192  
 Pro Lys Gly Leu Phe Pro Pro Glu Pro Glu His Tyr Arg Gly Pro Lys  
 50 55 60

25 ctt aaa gtg gct atc att gga gct ggg ctc gct ggc atg tca act gca 240  
 Leu Lys Val Ala Ile Ile Gly Ala Gly Leu Ala Gly Met Ser Thr Ala  
 65 70 75 80

gtg gag ctt ttg gat caa ggg cat gag gtt gac ata tat gaa tcc aga 288  
 Val Glu Leu Leu Asp Gln Gly His Glu Val Asp Ile Tyr Glu Ser Arg  
 85 90 95

30 caa ttt att ggt ggt aaa gtc ggt tct ttt gta gat aag cgt gga aac 336  
 Gln Phe Ile Gly Gly Lys Val Gly Ser Phe Val Asp Lys Arg Gly Asn  
 100 105 110

35 cat att gaa atg gga ctc cat gtg ttt ttt ggt tgc tat aac aat ctt 384  
 His Ile Glu Met Gly Leu His Val Phe Phe Gly Cys Tyr Asn Asn Leu  
 115 120 125

40 ttc aga ctt atg aaa aag gta ggt gca gat gaa aat tta ctg gtg aag 432  
 Phe Arg Leu Met Lys Lys Val Gly Ala Asp Glu Asn Leu Leu Val Lys  
 130 135 140

gat cat act cat acc ttt gta aac cga ggt gga gaa att ggt gaa ctt 480  
 Asp His Thr His Thr Phe Val Asn Arg Gly Gly Glu Ile Gly Glu Leu  
 145 150 155 160

45

214

	gat ttc cga ctt ccg atg ggt gca cca tta cat ggt att cgt gca ttt Asp Phe Arg Leu Pro Met Gly Ala Pro Leu His Gly Ile Arg Ala Phe 165 170 175	528
5	cta aca act aat caa ctg aag cct tat gat aaa gca agg aat gct gtg Leu Thr Thr Asn Gln Leu Lys Pro Tyr Asp Lys Ala Arg Asn Ala Val 180 185 190	576
10	gct ctt gcc ctt agc cca gtt gta cgt gct ctt att gat cca aat ggt Ala Leu Ala Leu Ser Pro Val Val Arg Ala Leu Ile Asp Pro Asn Gly 195 200 205	624
15	gca atg cag gat ata agg aac tta gat aat att agc ttt tct gat tgg Ala Met Gln Asp Ile Arg Asn Leu Asp Asn Ile Ser Phe Ser Asp Trp 210 215 220	672
20	ttc tta tcc aaa ggc ggt acc cgc atg agc atc caa agg atg tgg gat Phe Leu Ser Lys Gly Gly Thr Arg Met Ser Ile Gln Arg Met Trp Asp 225 230 235 240	720
	cca gtt gct tat gcc ctc gga ttt att gac tgt gat aat atc agt gcc Pro Val Ala Tyr Ala Leu Gly Phe Ile Asp Cys Asp Asn Ile Ser Ala 245 250 255	768
25	cgt tgt atg ctt act ata ttt tct cta ttt gct act aag aca gaa gct Arg Cys Met Leu Thr Ile Phe Ser Leu Phe Ala Thr Lys Thr Glu Ala 260 265 270	816
30	tct ctg ttg cgt atg ttg aag ggt tcg cct gat gtt tac tta agc ggt Ser Leu Leu Arg Met Leu Lys Gly Ser Pro Asp Val Tyr Leu Ser Gly 275 280 285	864
35	cct ata aga aag tat att aca gat aaa ggt gga agg ttt cac cta agg Pro Ile Arg Lys Tyr Ile Thr Asp Lys Gly Gly Arg Phe His Leu Arg 290 295 300	912
40	tgg ggg tgt aga gag ata ctt tat gat gaa cta tca aat ggc gac aca Trp Gly Cys Arg Glu Ile Leu Tyr Asp Glu Leu Ser Asn Gly Asp Thr 305 310 315 320	960
	tat atc aca ggc att gca atg tcg aag gct acc aat aaa aaa ctt gtg Tyr Ile Thr Gly Ile Ala Met Ser Lys Ala Thr Asn Lys Lys Leu Val 325 330 335	1008
45	aaa gct gac gtg tat gtt gca gca tgt gat gtt cct gga ata aaa agg	1056

## 215

	Lys Ala Asp Val Tyr Val Ala Ala Cys Asp Val Pro Gly Ile Lys Arg	
	340 345 350	
5	ttg atc cca tcg gag tgg aga gaa tgg gat cta ttt gac aat atc tat Leu Ile Pro Ser Glu Trp Arg Glu Trp Asp Leu Phe Asp Asn Ile Tyr	1104
	355 360 365	
10	aaa cta gtt gga gtt cca gtt gtc act gtt cag ctt agg tac aat ggt Lys Leu Val Gly Val Pro Val Val Thr Val Gln Leu Arg Tyr Asn Gly	1152
	370 375 380	
15	tgg gtg aca gag atg caa gat ctg gaa aaa tca agg cag ttg aga gct Trp Val Thr Glu Met Gln Asp Leu Glu Lys Ser Arg Gln Leu Arg Ala	1200
	385 390 395 400	
20	gca gta gga ttg gat aat ctt ctt tat act cca gat gca gac ttt tct Ala Val Gly Leu Asp Asn Leu Leu Tyr Thr Pro Asp Ala Asp Phe Ser	1248
	405 410 415	
25	tgt ttt tct gat ctt gca ctc tcg tcg cct gaa gat tat tat att gaa Cys Phe Ser Asp Leu Ala Leu Ser Ser Pro Glu Asp Tyr Tyr Ile Glu	1296
	420 425 430	
30	gga caa ggg tcc cta ata cag gct gtt ctc acg cca ggg gat cca tac Gly Gln Gly Ser Leu Ile Gln Ala Val Leu Thr Pro Gly Asp Pro Tyr	1344
	435 440 445	
35	atg ccc cta cct aat gat gca att ata gaa aga gtt cgg aaa cag gtt Met Pro Leu Pro Asn Asp Ala Ile Ile Glu Arg Val Arg Lys Gln Val	1392
	450 455 460	
40	ttg gat tta ttc cca tcc tct caa ggc ctg gaa gtt cta tgg tct tcg Leu Asp Leu Phe Pro Ser Ser Gln Gly Leu Glu Val Leu Trp Ser Ser	1440
	465 470 475 480	
45	gtg gtt aaa atc gga caa tcc cta tat cgg gag ggg cct gga aag gac Val Val Lys Ile Gly Gln Ser Leu Tyr Arg Glu Gly Pro Gly Lys Asp	1488
	485 490 495	
50	cca ttc aga cct gat cag aag aca cca gta aaa aat ttc ttc ctt gca Pro Phe Arg Pro Asp Gln Lys Thr Pro Val Lys Asn Phe Phe Leu Ala	1536
	500 505 510	
55	ggg tca tac acc aaa cag gat tac att gac agt atg gaa gga gcg acc Gly Ser Tyr Thr Lys Gln Asp Tyr Ile Asp Ser Met Glu Gly Ala Thr	1584

	515	520	525	
	cta tcg ggg aga caa gca gct gca tat atc tgc agc gcc ggt gaa gat			1632
	Leu Ser Gly Arg Gln Ala Ala Ala Tyr Ile Cys Ser Ala Gly Glu Asp			
5	530	535	540	
	ctg gca gca ctt cgc aag aag atc gct gct gat cat cca gag caa ctg			1680
	Leu Ala Ala Leu Arg Lys Lys Ile Ala Ala Asp His Pro Glu Gln Leu			
	545	550	555	560
10	atc aac aaa gat tct aac gtg tcg gat gaa ctg agt ctc gta taa			1725
	Ile Asn Lys Asp Ser Asn Val Ser Asp Glu Leu Ser Leu Val			
	565	570		
15	<210> 132			
	<211> 574			
20	<212> PRT			
	<213> Narcissus pseudonarcissus			
25	<400> 132			
	Met Ala Ser Ser Thr Cys Leu Ile His Ser Ser Ser Phe Gly Val Gly			
	1	5	10	15
30	Gly Lys Lys Val Lys Met Asn Thr Met Ile Arg Ser Lys Leu Phe Ser			
	20	25	30	
35	Ile Arg Ser Ala Leu Asp Thr Lys Val Ser Asp Met Ser Val Asn Ala			
	35	40	45	
40	Pro Lys Gly Leu Phe Pro Pro Glu Pro Glu His Tyr Arg Gly Pro Lys			
	50	55	60	
45	Leu Lys Val Ala Ile Ile Gly Ala Gly Leu Ala Gly Met Ser Thr Ala			
	65	70	75	80

Val Glu Leu Leu Asp Gln Gly His Glu Val Asp Ile Tyr Glu Ser Arg  
 85 90 95  
 5

Gln Phe Ile Gly Gly Lys Val Gly Ser Phe Val Asp Lys Arg Gly Asn  
 100 105 110

10 His Ile Glu Met Gly Leu His Val Phe Phe Gly Cys Tyr Asn Asn Leu  
 115 120 125

15 Phe Arg Leu Met Lys Lys Val Gly Ala Asp Glu Asn Leu Leu Val Lys  
 130 135 140

20 Asp His Thr His Thr Phe Val Asn Arg Gly Gly Glu Ile Gly Glu Leu  
 145 150 155 160

25 Asp Phe Arg Leu Pro Met Gly Ala Pro Leu His Gly Ile Arg Ala Phe  
 165 170 175

Leu Thr Thr Asn Gln Leu Lys Pro Tyr Asp Lys Ala Arg Asn Ala Val  
 180 185 190

30 Ala Leu Ala Leu Ser Pro Val Val Arg Ala Leu Ile Asp Pro Asn Gly  
 195 200 205

35 Ala Met Gln Asp Ile Arg Asn Leu Asp Asn Ile Ser Phe Ser Asp Trp  
 210 215 220

40 Phe Leu Ser Lys Gly Gly Thr Arg Met Ser Ile Gln Arg Met Trp Asp  
 225 230 235 240

Pro Val Ala Tyr Ala Leu Gly Phe Ile Asp Cys Asp Asn Ile Ser Ala  
 245 250 255  
 45

Arg Cys Met Leu Thr Ile Phe Ser Leu Phe Ala Thr Lys Thr Glu Ala  
 260 265 270

5

Ser Leu Leu Arg Met Leu Lys Gly Ser Pro Asp Val Tyr Leu Ser Gly  
 275 280 285

10

Pro Ile Arg Lys Tyr Ile Thr Asp Lys Gly Gly Arg Phe His Leu Arg  
 290 295 300

15

Trp Gly Cys Arg Glu Ile Leu Tyr Asp Glu Leu Ser Asn Gly Asp Thr  
 305 310 315 320

20

Tyr Ile Thr Gly Ile Ala Met Ser Lys Ala Thr Asn Lys Lys Leu Val  
 325 330 335

Lys Ala Asp Val Tyr Val Ala Ala Cys Asp Val Pro Gly Ile Lys Arg  
 340 345 350

25

Leu Ile Pro Ser Glu Trp Arg Glu Trp Asp Leu Phe Asp Asn Ile Tyr  
 355 360 365

30

Lys Leu Val Gly Val Pro Val Val Thr Val Gln Leu Arg Tyr Asn Gly  
 370 375 380

35

Trp Val Thr Glu Met Gln Asp Leu Glu Lys Ser Arg Gln Leu Arg Ala  
 385 390 395 400

40

Ala Val Gly Leu Asp Asn Leu Leu Tyr Thr Pro Asp Ala Asp Phe Ser  
 405 410 415

45

Cys Phe Ser Asp Leu Ala Leu Ser Ser Pro Glu Asp Tyr Tyr Ile Glu  
 420 425 430

## 219

Gly Gln Gly Ser Leu Ile Gln Ala Val Leu Thr Pro Gly Asp Pro Tyr  
 435 440 445

5 Met Pro Leu Pro Asn Asp Ala Ile Ile Glu Arg Val Arg Lys Gln Val  
 450 455 460

10 Leu Asp Leu Phe Pro Ser Ser Gln Gly Leu Glu Val Leu Trp Ser Ser  
 465 470 475 480

15 Val Val Lys Ile Gly Gln Ser Leu Tyr Arg Glu Gly Pro Gly Lys Asp  
 485 490 495

Pro Phe Arg Pro Asp Gln Lys Thr Pro Val Lys Asn Phe Phe Leu Ala  
 500 505 510

20 Gly Ser Tyr Thr Lys Gln Asp Tyr Ile Asp Ser Met Glu Gly Ala Thr  
 515 520 525

25 Leu Ser Gly Arg Gln Ala Ala Ala Tyr Ile Cys Ser Ala Gly Glu Asp  
 530 535 540

30 Leu Ala Ala Leu Arg Lys Lys Ile Ala Ala Asp His Pro Glu Gln Leu  
 545 550 555 560

Ile Asn Lys Asp Ser Asn Val Ser Asp Glu Leu Ser Leu Val  
 565 570

35

&lt;210&gt; 133

&lt;211&gt; 1848

40

&lt;212&gt; DNA

&lt;213&gt; Lycopersicon esculentum

&lt;220&gt;

5 &lt;221&gt; CDS

&lt;222&gt; (1)..(1848)

&lt;223&gt;

10

&lt;400&gt; 133

15 atg tgt acc ttg agt ttt atg tat cct aat tca ctt ctt gat ggt acc 48  
Met Cys Thr Leu Ser Phe Met Tyr Pro Asn Ser Leu Leu Asp Gly Thr  
1 5 10 15

20 tgc aag act gta gct ttg ggt gat agc aaa cca aga tac aat aaa cag 96  
Cys Lys Thr Val Ala Leu Gly Asp Ser Lys Pro Arg Tyr Asn Lys Gln  
20 25 30

25 aga agt tct tgt ttt gac cct ttg ata att gga aat tgt act gat cag 144  
Arg Ser Ser Cys Phe Asp Pro Leu Ile Ile Gly Asn Cys Thr Asp Gln  
35 40 45

cag cag ctt tgt ggc ttg agt tgg ggg gtg gac aag gct aag gga aga 192  
Gln Gln Leu Cys Gly Leu Ser Trp Gly Val Asp Lys Ala Lys Gly Arg  
50 55 60

30 aga ggg ggt act gtt tcc aat ttg aaa gca gtt gta gat gta gac aaa 240  
Arg Gly Gly Thr Val Ser Asn Leu Lys Ala Val Val Asp Val Asp Lys  
65 70 75 80

35 aga gtg gag agc tat ggc agt agt gat gta gaa gga aat gag agt ggc 288  
Arg Val Glu Ser Tyr Gly Ser Ser Asp Val Glu Gly Asn Glu Ser Gly  
85 90 95

40 agc tat gat gcc att gtt ata ggt tca gga ata ggt gga ttg gtg gca 336  
Ser Tyr Asp Ala Ile Val Ile Gly Ser Gly Ile Gly Gly Leu Val Ala  
100 105 110

gcg acg cag ctg gcg gtt aag gga gct aag gtt tta gtt ctg gag aag 384  
Ala Thr Gln Leu Ala Val Lys Gly Ala Lys Val Leu Val Leu Glu Lys  
115 120 125

45



## 221

	tat gtt att cct ggt gga agc tct ggc ttt tac gag agg gat ggt tat	432
	Tyr Val Ile Pro Gly Gly Ser Ser Gly Phe Tyr Glu Arg Asp Gly Tyr	
	130 135 140	
5	aag ttt gat gtt ggt tca tca gtg atg ttt gga ttc agt gat aag gga	480
	Lys Phe Asp Val Gly Ser Ser Val Met Phe Gly Phe Ser Asp Lys Gly	
	145 150 155 160	
10	aac ctc aat tta att act caa gca ttg gca gca gta gga cgt aaa tta	528
	Asn Leu Asn Leu Ile Thr Gln Ala Leu Ala Ala Val Gly Arg Lys Leu	
	165 170 175	
15	gaa gtt ata cct gac cca aca act gta cat ttc cac ctg cca aat gac	576
	Glu Val Ile Pro Asp Pro Thr Thr Val His Phe His Leu Pro Asn Asp	
	180 185 190	
20	ctt tct gtt cgt ata cac cga gag tat gat gac ttc att gaa gag ctt	624
	Leu Ser Val Arg Ile His Arg Glu Tyr Asp Asp Phe Ile Glu Glu Leu	
	195 200 205	
	gtg agt aaa ttt cca cat gaa aag gaa ggg att atc aaa ttt tac agt	672
	Val Ser Lys Phe Pro His Glu Lys Glu Gly Ile Ile Lys Phe Tyr Ser	
	210 215 220	
25	gaa tgc tgg aag atc ttt aat tct ctg aat tca ttg gaa ctg aag tct	720
	Glu Cys Trp Lys Ile Phe Asn Ser Leu Asn Ser Leu Glu Leu Lys Ser	
	225 230 235 240	
30	ttg gag gaa ccc atc tac ctt ttt ggc cag ttc ttt aag aag ccc ctt	768
	Leu Glu Glu Pro Ile Tyr Leu Phe Gly Gln Phe Phe Lys Lys Pro Leu	
	245 250 255	
35	gaa tgc ttg act ctt gcc tac tat ttg ccc cag aat gct ggt agc atc	816
	Glu Cys Leu Thr Leu Ala Tyr Tyr Leu Pro Gln Asn Ala Gly Ser Ile	
	260 265 270	
40	gct cgg aag tat ata aga gat cct ggg ttg ctg tct ttt ata gat gca	864
	Ala Arg Lys Tyr Ile Arg Asp Pro Gly Leu Leu Ser Phe Ile Asp Ala	
	275 280 285	
	gag tgc ttt atc gtg agt aca gtt aat gca tta caa aca cca atg atc	912
	Glu Cys Phe Ile Val Ser Thr Val Asn Ala Leu Gln Thr Pro Met Ile	
	290 295 300	
45	aat gca agc atg gtt cta tgt gac aga cat ttt ggc gga atc aac tac	960

222

[illegible]

## 223

	485	490	495	
5	agg att ata agc aga ctt gaa aaa aca ctc ttc cca ggg ctt aag tca Arg Ile Ile Ser Arg Leu Glu Lys Thr Leu Phe Pro Gly Leu Lys Ser	500	505	510
10	tct att ctc ttt aag gag gtg gga act cca aag acc cac aga cga tac Ser Ile Leu Phe Lys Glu Val Gly Thr Pro Lys Thr His Arg Arg Tyr	515	520	525
15	ctt gct cgt gat agt ggt acc tat gga cca atg cca cgc gga aca cct Leu Ala Arg Asp Ser Gly Thr Tyr Gly Pro Met Pro Arg Gly Thr Pro	530	535	540
20	aag gga ctc ctg gga atg cct ttc aat acc act gct ata gat ggt cta Lys Gly Leu Leu Gly Met Pro Phe Asn Thr Thr Ala Ile Asp Gly Leu	545	550	555
25	tat tgt gtt ggc gat agt tgc ttc cca gga caa ggt gtt ata gct gta Tyr Cys Val Gly Asp Ser Cys Phe Pro Gly Gln Gly Val Ile Ala Val	565	570	575
30	gcc ttt tca gga gta atg tgc gct cat cgt gtt gca gct gac tta ggg Ala Phe Ser Gly Val Met Cys Ala His Arg Val Ala Ala Asp Leu Gly	580	585	590
35	ttt gaa aaa aaa tca gat gtg ctg gac agt gct ctt ctt aga cta ctt Phe Glu Lys Lys Ser Asp Val Leu Asp Ser Ala Leu Leu Arg Leu Leu	595	600	605
40	ggt tgg tta agg aca cta gca tga Gly Trp Leu Arg Thr Leu Ala	610	615	
45	<210> 134 <211> 615 <212> PRT <213> Lycopersicon esculentum			

&lt;400&gt; 134

Met Cys Thr Leu Ser Phe Met Tyr Pro Asn Ser Leu Leu Asp Gly Thr  
 1 5 10 15

5

Cys Lys Thr Val Ala Leu Gly Asp Ser Lys Pro Arg Tyr Asn Lys Gln  
 20 25 30

10

Arg Ser Ser Cys Phe Asp Pro Leu Ile Ile Gly Asn Cys Thr Asp Gln  
 35 40 45

15

Gln Gln Leu Cys Gly Leu Ser Trp Gly Val Asp Lys Ala Lys Gly Arg  
 50 55 60

20

Arg Gly Gly Thr Val Ser Asn Leu Lys Ala Val Val Asp Val Asp Lys  
 65 70 75 80

Arg Val Glu Ser Tyr Gly Ser Ser Asp Val Glu Gly Asn Glu Ser Gly  
 85 90 95

25

Ser Tyr Asp Ala Ile Val Ile Gly Ser Gly Ile Gly Gly Leu Val Ala  
 100 105 110

30

Ala Thr Gln Leu Ala Val Lys Gly Ala Lys Val Leu Val Leu Glu Lys  
 115 120 125

35

Tyr Val Ile Pro Gly Gly Ser Ser Gly Phe Tyr Glu Arg Asp Gly Tyr  
 130 135 140

40

Lys Phe Asp Val Gly Ser Ser Val Met Phe Gly Phe Ser Asp Lys Gly  
 145 150 155 160

Asn Leu Asn Leu Ile Thr Gln Ala Leu Ala Ala Val Gly Arg Lys Leu  
 165 170 175

45

225

Glu Val Ile Pro Asp Pro Thr Thr Val His Phe His Leu Pro Asn Asp  
 180 185 190

5

Leu Ser Val Arg Ile His Arg Glu Tyr Asp Asp Phe Ile Glu Glu Leu  
 195 200 205

10

Val Ser Lys Phe Pro His Glu Lys Glu Gly Ile Ile Lys Phe Tyr Ser  
 210 215 220

15

Glu Cys Trp Lys Ile Phe Asn Ser Leu Asn Ser Leu Glu Leu Lys Ser  
 225 230 235 240

20

Leu Glu Glu Pro Ile Tyr Leu Phe Gly Gln Phe Phe Lys Lys Pro Leu  
 245 250 255

Glu Cys Leu Thr Leu Ala Tyr Tyr Leu Pro Gln Asn Ala Gly Ser Ile  
 260 265 270

25

Ala Arg Lys Tyr Ile Arg Asp Pro Gly Leu Leu Ser Phe Ile Asp Ala  
 275 280 285

30

Glu Cys Phe Ile Val Ser Thr Val Asn Ala Leu Gln Thr Pro Met Ile  
 290 295 300

35

Asn Ala Ser Met Val Leu Cys Asp Arg His Phe Gly Gly Ile Asn Tyr  
 305 310 315 320

40

Pro Val Gly Gly Val Gly Glu Ile Ala Lys Ser Leu Ala Lys Gly Leu  
 325 330 335

Asp Asp His Gly Ser Gln Ile Leu Tyr Arg Ala Asn Val Thr Ser Ile  
 340 345 350

45

## 226

Ile Leu Asp Asn Gly Lys Ala Val Gly Val Lys Leu Ser Asp Gly Arg  
 355 360 365

5 Lys Phe Tyr Ala Lys Thr Ile Val Ser Asn Ala Thr Arg Trp Asp Thr  
 370 375 380

10 Phe Gly Lys Leu Leu Lys Ala Glu Asn Leu Pro Lys Glu Glu Glu Asn  
 385 390 395 400

15 Phe Gln Lys Ala Tyr Val Lys Ala Pro Ser Phe Leu Ser Ile His Met  
 405 410 415

20 Gly Val Lys Ala Asp Val Leu Pro Pro Asp Thr Asp Cys His His Phe  
 420 425 430

25 Phe Leu Ser Ile Pro Thr Val Leu Asp Ser Ser Leu Ala Pro Glu Gly  
 450 455 460

30 His His Ile Leu His Ile Phe Thr Thr Ser Ser Ile Glu Asp Trp Glu  
 465 470 475 480

35 Gly Leu Ser Pro Lys Asp Tyr Glu Ala Lys Lys Glu Val Val Ala Glu  
 485 490 495

40 Arg Ile Ile Ser Arg Leu Glu Lys Thr Leu Phe Pro Gly Leu Lys Ser  
 500 505 510

45 Ser Ile Leu Phe Lys Glu Val Gly Thr Pro Lys Thr His Arg Arg Tyr  
 515 520 525

Leu Ala Arg Asp Ser Gly Thr Tyr Gly Pro Met Pro Arg Gly Thr Pro

227

530

535

540

5 Lys Gly Leu Leu Gly Met Pro Phe Asn Thr Thr Ala Ile Asp Gly Leu  
545 550 555 560

10 Tyr Cys Val Gly Asp Ser Cys Phe Pro Gly Gln Gly Val Ile Ala Val  
565 570 575

15 Ala Phe Ser Gly Val Met Cys Ala His Arg Val Ala Ala Asp Leu Gly  
580 585 590

Phe Glu Lys Lys Ser Asp Val Leu Asp Ser Ala Leu Leu Arg Leu Leu  
595 600 605

20 Gly Trp Leu Arg Thr Leu Ala  
610 615

25 <210> 135

<211> 1233

<212> DNA

30 <213> Tagetes erecta

35 <220>

<221> CDS

<222> (1)..(1233)

40 <223>

45 <400> 135  
atg gcc aca cac aaa ctc ctt caa ttc acc acc aat ctc cca cca tct

[illegible]



	180	185	190	
	gcg tta gag gct att gag aag ctg caa aag aac gtt gac aca ctt ata			624
	Ala Leu Glu Ala Ile Glu Lys Leu Gln Lys Asn Val Asp Thr Leu Ile			
5	195	200	205	
	gtg att cca aat gac cgt ttg ctg gat att gct gat gaa aac acg cct			672
	Val Ile Pro Asn Asp Arg Leu Leu Asp Ile Ala Asp Glu Asn Thr Pro			
	210	215	220	
10				
	ctt cag gat gct ttt ctt ctt gct gat gat gta ctc cgc caa gga gtt			720
	Leu Gln Asp Ala Phe Leu Leu Ala Asp Asp Val Leu Arg Gln Gly Val			
	225	230	235	240
	caa gga atc tca gat ata att aca ata cct ggg ctg gta aat gtg gac			768
15	Gln Gly Ile Ser Asp Ile Ile Thr Ile Pro Gly Leu Val Asn Val Asp			
	245	250	255	
	ttt gca gac gtt aaa gca gtc atg aaa gat tct gga act gca atg ctt			816
20	Phe Ala Asp Val Lys Ala Val Met Lys Asp Ser Gly Thr Ala Met Leu			
	260	265	270	
	ggc gtc ggt gtt tcc tca agt aaa aac cga gct gaa gaa gca gct gaa			864
	Gly Val Gly Val Ser Ser Ser Lys Asn Arg Ala Glu Glu Ala Ala Glu			
25	275	280	285	
	caa gca act ctt gct cct ttg att gga tca tca att caa tct gct aca			912
	Gln Ala Thr Leu Ala Pro Leu Ile Gly Ser Ser Ile Gln Ser Ala Thr			
	290	295	300	
30				
	ggc gtt gtt tat aat att acc gga ggg aag gac ata act cta caa gaa			960
	Gly Val Val Tyr Asn Ile Thr Gly Gly Lys Asp Ile Thr Leu Gln Glu			
	305	310	315	320
	gtc aac agg gtt tct cag gtg gta aca agt ttg gca gat cca tca gca			1008
35	Val Asn Arg Val Ser Gln Val Val Thr Ser Leu Ala Asp Pro Ser Ala			
	325	330	335	
	aac att ata ttc ggg gca gtg gta gat gag aga tac aac ggg gag att			1056
40	Asn Ile Ile Phe Gly Ala Val Val Asp Glu Arg Tyr Asn Gly Glu Ile			
	340	345	350	
	cat gtg acc att gtt gct act ggc ttt gcc cag tcg ttt cag aaa tct			1104
	His Val Thr Ile Val Ala Thr Gly Phe Ala Gln Ser Phe Gln Lys Ser			
45	355	360	365	

ctt ctt gct gac ccg aaa gga gca aaa ctt gtt gat aga aat caa gaa 1152  
 Leu Leu Ala Asp Pro Lys Gly Ala Lys Leu Val Asp Arg Asn Gln Glu  
 370 375 380

5 cct aca caa cct ttg act tcc gcg aga tct ttg aca aca cct tct ect 1200  
 Pro Thr Gln Pro Leu Thr Ser Ala Arg Ser Leu Thr Thr Pro Ser Pro  
 385 390 395 400

10 gct ccg tct ccg tct agg aaa ctc ttc ttt taa 1233  
 Ala Pro Ser Arg Ser Arg Lys Leu Phe Phe  
 405 410

15 <210> 136  
 <211> 410  
 <212> PRT  
 20 <213> Tagetes erecta

25 <400> 136  
 Met Ala Thr His Lys Leu Leu Gln Phe Thr Thr Asn Leu Pro Pro Ser  
 1 5 10 15

30 Ser Ser Ser Ile Ser Thr Gly Cys Ser Leu Ser Pro Phe Phe Leu Lys  
 20 25 30

35 Ser Ser Ser His Ser Pro Asn Pro Arg Arg His Arg Arg Ser Ala Val  
 35 40 45

40 Cys Cys Ser Phe Ala Ser Leu Asp Ser Ala Lys Ile Lys Val Val Gly  
 50 55 60

45 Val Gly Gly Gly Gly Asn Asn Ala Val Asn Arg Met Ile Gly Ser Gly  
 65 70 75 80

231

Leu Gln Gly. Val Asp Phe Tyr Ala Ile Ash Thr Asp Ser Gln Ala Leu  
85 90 95

5

Leu Gln Ser Val Ala His Asn Pro Ile Gln Ile Gly Glu Leu Leu Thr  
100 105 110

10 Arg Gly Leu Gly Thr Gly Gly Asn Pro Leu Leu Gly Glu Gln Ala Ala  
115 120 125

Glu Glu Ser Lys Glu Ala Ile Gly Asn Ala Leu Lys Gly Ser Asp Leu  
15            130                 135                         140

Val Phe Ile Thr Ala Gly Met Gly Gly Gly Thr Gly Ser Gly Ala Ala  
145 150 155 160

Pro Val Val Ala Gln Ile Ala Lys Glu Ala Gly Tyr Leu Thr Val Gly  
165 170 175

25

Val Val Thr Tyr Pro Phe Ser Phe Glu Gly Arg Lys Arg Ser Val Gln  
180 185 190

30 Ala Leu Glu Ala Ile Glu Lys Leu Gln Lys Asn Val. Asp Thr Leu Ile  
195 200 205

Val Ile Pro Asn Asp Arg Leu Leu Asp Ile Ala Asp Glu Asn Thr Pro  
35            210                    215                    220

Leu Gln Asp Ala Phe Leu Leu Ala Asp Asp Val Leu Arg Gln Gly Val  
225                    230                    235                    240

Gln Gly Ile Ser Asp Ile Ile Thr Ile Pro Gly Leu Val Asn Val Asp  
245 250 255

45

## 232

Phe Ala Asp Val Lys Ala Val Met Lys Asp Ser Gly Thr Ala Met Leu  
 260 265 270

5 Gly Val Gly Val Ser Ser Ser Lys Asn Arg Ala Glu Glu Ala Ala Glu  
 275 280 285

10 Gln Ala Thr Leu Ala Pro Leu Ile Gly Ser Ser Ile Gln Ser Ala Thr  
 290 295 300

15 Gly Val Val Tyr Asn Ile Thr Gly Gly Lys Asp Ile Thr Leu Gln Glu  
 305 310 315 320

Val Asn Arg Val Ser Gln Val Val Thr Ser Leu Ala Asp Pro Ser Ala  
 325 330 335

20 Asn Ile Ile Phe Gly Ala Val Val Asp Glu Arg Tyr Asn Gly Glu Ile  
 340 345 350

25 His Val Thr Ile Val Ala Thr Gly Phe Ala Gln Ser Phe Gln Lys Ser  
 355 360 365

30 Leu Leu Ala Asp Pro Lys Gly Ala Lys Leu Val Asp Arg Asn Gln Glu  
 370 375 380

35 Pro Thr Gln Pro Leu Thr Ser Ala Arg Ser Leu Thr Thr Pro Ser Pro  
 385 390 395 400

Ala Pro Ser Arg Ser Arg Lys Leu Phe Phe  
 405 410

40 <210> 137

<211> 891

&lt;212&gt; DNA

&lt;213&gt; Tagetes erecta

5

&lt;220&gt;

&lt;221&gt; CDS

10

&lt;222&gt; (1)..(891)

&lt;223&gt;

15

&lt;400&gt; 137

atg aca tcc ctg agg, ttt cta aca gaa ccc tca ctt gta tgc tca tcc 48  
 Met Thr Ser Leu Arg Phe Leu Thr Glu Pro Ser Leu Val Cys Ser Ser  
 20 1 5 10 15

act ttc ccc aca ttc aat ccc cta cac aaa acc cta act aaa cca aca 96  
 Thr Phe Pro Thr Phe Asn Pro Leu His Lys Thr Leu Thr Lys Pro Thr  
 20 25 30

cca aaa ccc tac cca aag cca cca cca att cgc tcc gtc ctt caa tac 144  
 Pro Lys Pro Tyr Pro Lys Pro Pro Pro Ile Arg Ser Val Leu Gln Tyr  
 35 40 45

aat cgc aaa cca gag ctc gcc gga gac act cca cga gtc gtc gca atc 192  
 Asn Arg Lys Pro Glu Leu Ala Gly Asp Thr Pro Arg Val Val Ala Ile  
 50 55 60

gac gcc gac gtt ggt cta cgt aac ctc gat ctt ctt ctc ggt ctc gaa 240  
 Asp Ala Asp Val Gly Leu Arg Asn Leu Asp Leu Leu Leu Gly Leu Glu  
 65 70 75 80

aac cgc gtc aat tac acc gtc gtt gaa gtt ctc aac ggc gat tgc aga 288  
 Asn Arg Val Asn Tyr Thr Val Val Glu Val Leu Asn Gly Asp Cys Arg  
 40 85 90 95

ctc gac caa gcc cta gtt cgt gat aaa cgc tgg tca aat ttc gaa ttg 336  
 Leu Asp Gln Ala Leu Val Arg Asp Lys Arg Trp Ser Asn Phe Glu Leu  
 100 105 110

45

## 234

	ctt tgt att tca aaa cct agg tca aaa ttg cct tta gga ttt ggg gga	384
	Leu Cys Ile Ser Lys Pro Arg Ser Lys Leu Pro Leu Gly Phe Gly Gly	
	115 120 125	
5	aaa gct tta gtt tgg ctt gat gca tta aaa gat agg caa gaa ggt tgc	432
	Lys Ala Leu Val Trp Leu Asp Ala Leu Lys Asp Arg Gln Glu Gly Cys	
	130 135 140	
10	ccg gat ttt ata ctt ata gat tgt cct gca ggt att gat gcc ggg ttc	480
	Pro Asp Phe Ile Leu Ile Asp Cys Pro Ala Gly Ile Asp Ala Gly Phe	
	145 150 155 160	
	ata acc gcc att aca ccg gct aac gaa gcc gta tta gtt aca aca cct	528
15	Ile Thr Ala Ile Thr Pro Ala Asn Glu Ala Val Leu Val Thr Thr Pro	
	165 170 175	
	gat att act gca ttg aga gat gca gat aga gtt aca ggc ttg ctt gaa	576
	Asp Ile Thr Ala Leu Arg Asp Ala Asp Arg Val Thr Gly Leu Leu Glu	
	180 185 190	
20	tgt gat gga att agg gat att aaa atg att gtg aac aga gtt aga act	624
	Cys Asp Gly Ile Arg Asp Ile Lys Met Ile Val Asn Arg Val Arg Thr	
	195 200 205	
25	gat ttg ata agg ggt gaa gat atg atg tca gtt ctt gat gtt caa gag	672
	Asp Leu Ile Arg Gly Glu Asp Met Met Ser Val Leu Asp Val Gln Glu	
	210 215 220	
30	atg ttg gga ttg tca ttg ttg agt gat acc cga gga ttc gaa gtg att	720
	Met Leu Gly Leu Ser Leu Leu Ser Asp Thr Arg Gly Phe Glu Val Ile	
	225 230 235 240	
	cgg agt acg aat aga ggg ttt ccg ctt gtg ttg aac aag cct ccg act	768
35	Arg Ser Thr Asn Arg Gly Phe Pro Leu Val Leu Asn Lys Pro Pro Thr	
	245 250 255	
	tta gca gga ttg gca ttt gag cag gct gct tgg aga ttg gtt gag caa	816
	Leu Ala Gly Leu Ala Phe Glu Gln Ala Ala Trp Arg Leu Val Glu Gln	
	260 265 270	
40	gat agc atg aag gct gtg atg gtg gag gaa gaa cct aaa aag agg gga	864
	Asp Ser Met Lys Ala Val Met Val Glu Glu Glu Pro Lys Lys Arg Gly	
	275 280 285	
45	ttt ttc tcg ttt ttt gga ggt tag tga	891

Phe Phe Ser Phe Phe Gly Gly  
 290 295

5 <210> 138

<211> 295

<212> PRT

10

<213> Tagetes erecta

15 <400> 138

Met Thr Ser Leu Arg Phe Leu Thr Glu Pro Ser Leu Val Cys Ser Ser  
 1 5 10 15

20

Thr Phe Pro Thr Phe Asn Pro Leu His Lys Thr Leu Thr Lys Pro Thr  
 20 25 30

25

Pro Lys Pro Tyr Pro Lys Pro Pro Pro Ile Arg Ser Val Leu Gln Tyr  
 35 40 45

30

Asn Arg Lys Pro Glu Leu Ala Gly Asp Thr Pro Arg Val Val Ala Ile  
 50 55 60

35

Asp Ala Asp Val Gly Leu Arg Asn Leu Asp Leu Leu Leu Gly Leu Glu  
 65 70 75 80

40

Asn Arg Val Asn Tyr Thr Val Val Glu Val Leu Asn Gly Asp Cys Arg  
 85 90 95

Leu Asp Gln Ala Leu Val Arg Asp Lys Arg Trp Ser Asn Phe Glu Leu  
 100 105 110

45

Leu Cys Ile Ser Lys Pro Arg Ser Lys Leu Pro Leu Gly Phe Gly Gly

	115	120	125
5	Lys Ala Leu Val Trp Leu Asp Ala Leu Lys Asp Arg Gln Glu Gly Cys		
	130	135	140
10	Pro Asp Phe Ile Leu Ile Asp Cys Pro Ala Gly Ile Asp Ala Gly Phe		
	145	150	155 160
	Ile Thr Ala Ile Thr Pro Ala Asn Glu Ala Val Leu Val Thr Thr Pro		
	165	170	175
15	Asp Ile Thr Ala Leu Arg Asp Ala Asp Arg Val Thr Gly Leu Leu Glu		
	180	185	190
20	Cys Asp Gly Ile Arg Asp Ile Lys Met Ile Val Asn Arg Val Arg Thr		
	195	200	205
25	Asp Leu Ile Arg Gly Glu Asp Met Met Ser Val Leu Asp Val Gln Glu		
	210	215	220
30	Met Leu Gly Leu Ser Leu Leu Ser Asp Thr Arg Gly Phe Glu Val Ile		
	225	230	235 240
	Arg Ser Thr Asn Arg Gly Phe Pro Leu Val Leu Asn Lys Pro Pro Thr		
	245	250	255
35	Leu Ala Gly Leu Ala Phe Glu Gln Ala Ala Trp Arg Leu Val Glu Gln		
	260	265	270
40	Asp Ser Met Lys Ala Val Met Val Glu Glu Glu Pro Lys Lys Arg Gly		
	275	280	285
45	Phe Phe Ser Phe Phe Gly Gly		
	290	295	



<210> 139

5 <211> 332

<212> DNA

<213> Tagetes erecta

10

<220>

15 <221> CDS

<222> (1) .. (330)

<223>

20

<400> 139

25 aag ctt gca cga gcc tct ctc tat ttt tac act tca atg gcg gca gca 48  
 Lys Leu Ala Arg Ala Ser Leu Tyr Phe Tyr Thr Ser Met Ala Ala Ala  
 1 5 10 15

30 att gct gtc cct tgt agc tca aga cca ttt ggc tta ggt cga atg cgg 96  
 Ile Ala Val Pro Cys Ser Ser Arg Pro Phe Gly Leu Gly Arg Met Arg  
 20 25 30

35 tta ctt ggt cat aaa ccc aca acc ata act tgt cac ttc ccc ttt tct 144  
 Leu Leu Gly His Lys Pro Thr Thr Ile Thr Cys His Phe Pro Phe Ser  
 35 40 45

40 ttt tct atc aaa tca ttt acc cca att gtt agg ggc aga aga tgt act 192  
 Phe Ser Ile Lys Ser Phe Thr Pro Ile Val Arg Gly Arg Arg Cys Thr  
 50 55 60

40 gtt tgt ttt gtt gcc ggt ggc gac agt aat agt aac agt aat aat aat 240  
 Val Cys Phe Val Ala Gly Gly Asp Ser Asn Ser Asn Ser Asn Asn Asn  
 65 70 75 80

45 agt gac agt aat agt aat aat ccg ggt ctg gat tta aac ccg gcg gtt 288  
 Ser Asp Ser Asn Ser Asn Asn Pro Gly Leu Asp Leu Asn Pro Ala Val

238

85

90

95

atg aac cgt aac cgt ttg gtt gaa gaa aaa atg gag agg tcg ac  
 Met Asn Arg Asn Arg Leu Val Glu Glu Lys Met Glu Arg Ser

332

5 100 105 110

<210> 140

10 <211> 110

<212> PRT

<213> Tagetes erecta

15

<400> 140

20 Lys Leu Ala Arg Ala Ser Leu Tyr Phe Tyr Thr Ser Met Ala Ala Ala  
 1 5 10 15

25 Ile Ala Val Pro Cys Ser Ser Arg Pro Phe Gly Leu Gly Arg Met Arg  
 20 25 30

30 Leu Leu Gly His Lys Pro Thr Thr Ile Thr Cys His Phe Pro Phe Ser  
 35 40 45

Phe Ser Ile Lys Ser Phe Thr Pro Ile Val Arg Gly Arg Arg Cys Thr  
 50 55 60

35 Val Cys Phe Val Ala Gly Gly Asp Ser Asn Ser Asn Ser Asn Asn Asn  
 65 70 75 80

40 Ser Asp Ser Asn Ser Asn Asn Pro Gly Leu Asp Leu Asn Pro Ala Val  
 85 90 95

45 Met Asn Arg Asn Arg Leu Val Glu Glu Lys Met Glu Arg Ser  
 100 105 110

<210> 141

5 <211> 332

<212> DNA

10 <213> Tagetes erceta

<220>

15 <221> misc\_feature

<222> (1)..(332)

20 <223>  $\beta$ -Hydroxylase Sense Fragment

<400> 141

25 aagcttgac gagcctctct ctatttttac acttcaatgg cggcagcaat tgctgtccct 60

tgtagctcaa gaccatttgg cttaggtcga atgcggttac ttggtcataa acccacaacc 120

ataacttgtc acttcccctt ttctttttct atcaaatcat ttaccccaat tgttaggggc 180

30 agaagatgta ctgtttgttt tgttgccggt ggcgacagta atagtaacag taataataat 240

agtgacagta atagtaataa tccgggtctg gatttaaacc cggcggttat gaaccgtaac 300

cgtttggttg aagaaaaaat ggagaggtcg ac 332

35

<210> 142

<211> 332

40 <212> DNA

<213> Tagetes erecta

&lt;220&gt;

5 &lt;221&gt; misc\_feature

&lt;222&gt; (1)..(332)

10 <223>  $\beta$ -Hydroxylase Antisense Fragment

&lt;400&gt; 142

15 gaattcggca cgagcctctc tctattttta cacttcaatg gcggcagcaa ttgctgtccc 60  
ttgtagctca agaccatttg gcttaggtcg aatgcggtta cttggtcata aaccacaac 120  
cataacttgt cacttccctt tttctttttc tatcaaatca tttaccccaa ttgttagggg 180  
20 cagaagatgt actgtttggt ttgttgccgg tggcgacagt aatagtaaca gtaataataa 240  
tagtgacagt aatagtaata atccgggtct ggatttaaac ccggcggtta tgaaccgtaa 300  
ccgtttggtt gaagaaaaaa tggagaggat cc 332

**This Page is Inserted by IFW Indexing and Scanning  
Operations and is not part of the Official Record**

**BEST AVAILABLE IMAGES**

Defective images within this document are accurate representations of the original documents submitted by the applicant.

Defects in the images include but are not limited to the items checked:

- ☐ BLACK BORDERS
- ☐ IMAGE CUT OFF AT TOP, BOTTOM OR SIDES
- ☐ FADED TEXT OR DRAWING
- ☒ BLURRED OR ILLEGIBLE TEXT OR DRAWING
- ☐ SKEWED/SLANTED IMAGES
- ☐ COLOR OR BLACK AND WHITE PHOTOGRAPHS
- ☐ GRAY SCALE DOCUMENTS
- ☒ LINES OR MARKS ON ORIGINAL DOCUMENT
- ☐ REFERENCE(S) OR EXHIBIT(S) SUBMITTED ARE POOR QUALITY
- ☐ OTHER: \_\_\_\_\_

**IMAGES ARE BEST AVAILABLE COPY.**

**As rescanning these documents will not correct the image problems checked, please do not report these problems to the IFW Image Problem Mailbox.**